STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 176925

TO: James Schultz **Location: 2d18 / 2c18** **Art Unit: 1635** **Monday, January 30, 2006** **Case Serial Number: 09/227881**	**From: Noble Jarrell** **Location: Biotech-Chem Library** **Rem 1B71** **Phone: 272-2556** **Noble.jarrell@uspto.gov**

Search Notes

STIC-Biotech/ChemLib 176925

From: Schultz, James
Sent: Wednesday, January 18, 2006 3:12 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 09/227,881

Hello,
Could you please run a score over length sequence search on SEQ ID NO:34 (5271 nt long), which returns hits between 50 and 500 nt long? I need only those hits that are 100% complementary. Please run the search in the interference databases as well.

Also, could you run a standard nucleotide sequence search on the full length of SEQ ID NO: 34, ONLY in the interference databases?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
Primary Examiner
AU 1635 (Biotechnology)
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

****
Searcher: Noble
Searcher Phone:
Date Searcher Picked up: 1/18/06
Date completed:
Searcher Prep Time: 45
Online Time: 10

****
Type of Search
NA# 1 AA#:
S/L: 1 Oligomer: 1
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

****
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: Compugen geneseq
WWW/Internet:
Other (Specify):

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 25, 2006, 20:57:13 ; Search time 603 Seconds
(without alignments)
15538.188 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagtttacctc.....tcgggcatgagccagcaagg 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

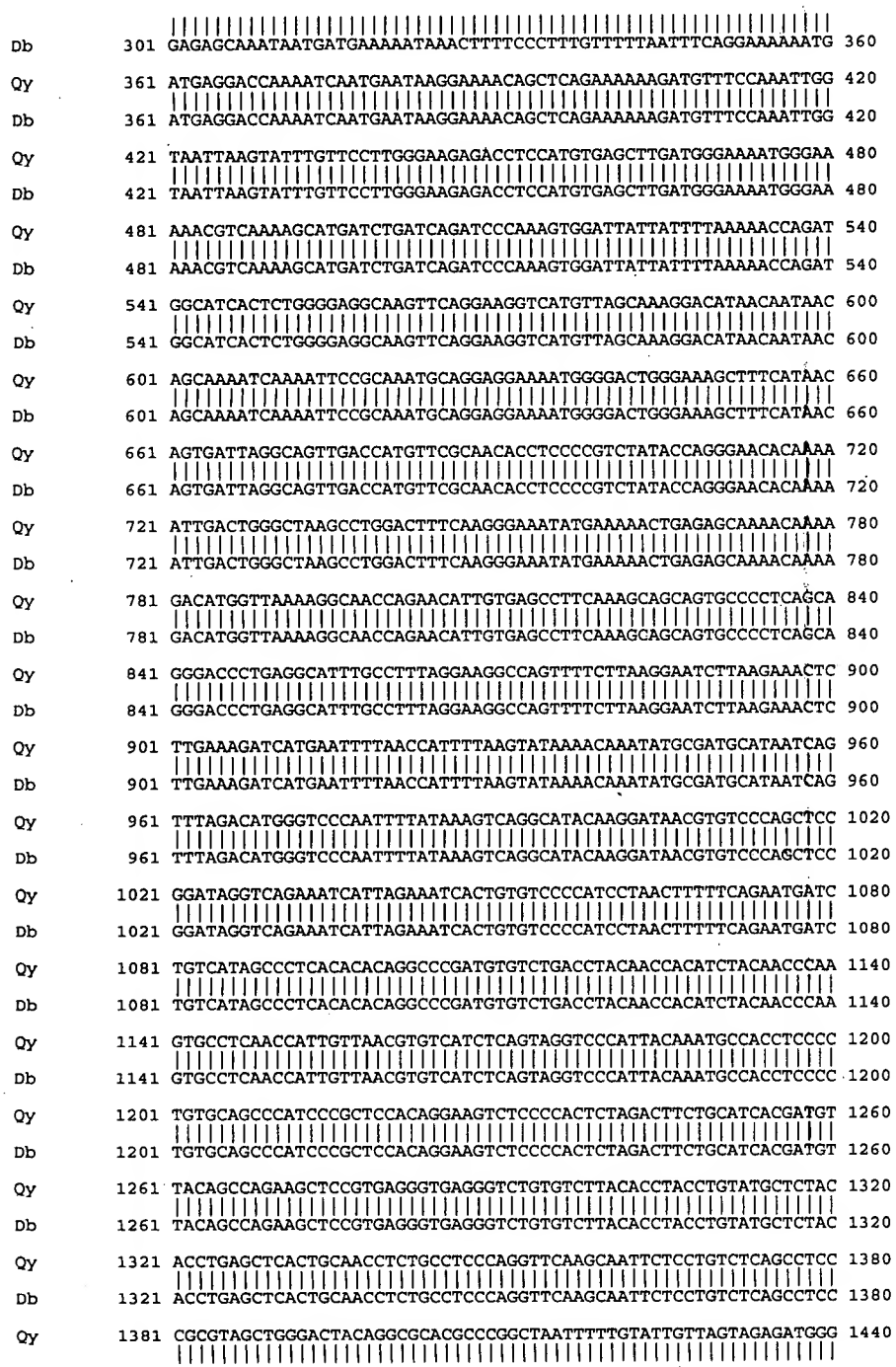
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5271	100.0	5271	3	US-09-306-828-34	Sequence 34, Appl
	2	5271	100.0	6169	3	US-08-938-669A-3	Sequence 3, Appli
	3	5271	100.0	6169	3	US-09-306-828-3	Sequence 3, Appli
	4	5246.4	99.5	5300	3	US-08-938-669A-1	Sequence 1, Appli
	5	5246.4	99.5	5300	3	US-09-306-828-1	Sequence 1, Appli
	6	5224.4	99.1	5304	3	US-08-938-669A-2	Sequence 2, Appli
	7	5224.4	99.1	5304	3	US-09-306-828-2	Sequence 2, Appli
	8	1804.4	34.2	2800	3	US-09-056-285A-1	Sequence 1, Appli
	9	1804.4	34.2	2800	3	US-10-017-870-10	Sequence 10, Appl
	10	1804.4	34.2	2800	3	US-09-952-464A-1	Sequence 1, Appli
	11	227	4.3	227	3	US-09-306-828-38	Sequence 38, Appl
	12	227	4.3	283	3	US-09-306-828-37	Sequence 37, Appl
c	13	189.8	3.6	29326	3	US-09-949-016-15356	Sequence 15356, A
c	14	184.6	3.5	205044	3	US-09-949-016-15851	Sequence 15851, A
c	15	184.6	3.5	205044	3	US-09-949-016-15852	Sequence 15852, A
c	16	184.6	3.5	205044	3	US-09-949-016-15853	Sequence 15853, A
c	17	184.6	3.5	223471	3	US-09-949-016-12387	Sequence 12387, A
c	18	184.6	3.5	223471	3	US-09-949-016-12724	Sequence 12724, A
c	19	184.6	3.5	223471	3	US-09-949-016-12725	Sequence 12725, A
c	20	184.4	3.5	1744	3	US-10-104-047-1845	Sequence 1845, Ap
c	21	183.2	3.5	88906	3	US-09-949-016-17468	Sequence 17468, A
	22	183	3.5	113966	3	US-09-949-016-12277	Sequence 12277, A
	23	183	3.5	113967	3	US-09-949-016-17051	Sequence 17051, A
c	24	182.8	3.5	601	3	US-09-949-016-102621	Sequence 102621,
c	25	182.8	3.5	601	3	US-09-949-016-102733	Sequence 102733,
	26	182.8	3.5	76164	3	US-09-949-016-12288	Sequence 12288, A
	27	182.8	3.5	76165	3	US-09-949-016-14005	Sequence 14005, A
c	28	182.6	3.5	601	3	US-09-949-016-185608	Sequence 185608,
	29	181.6	3.4	678533	3	US-09-949-016-14577	Sequence 14577, A
	30	181.6	3.4	678533	3	US-09-949-016-14578	Sequence 14578, A
	31	181.2	3.4	360470	3	US-09-949-016-13173	Sequence 13173, A
c	32	181	3.4	601	3	US-09-949-016-185607	Sequence 185607,
	33	181	3.4	13261	3	US-09-949-016-16870	Sequence 16870, A
c	34	181	3.4	44120	3	US-09-949-016-14151	Sequence 14151, A
c	35	181	3.4	44120	3	US-09-949-016-14152	Sequence 14152, A
c	36	181	3.4	44120	3	US-09-949-016-14153	Sequence 14153, A
c	37	181	3.4	44120	3	US-09-949-016-14154	Sequence 14154, A
c	38	181	3.4	44120	3	US-09-949-016-14155	Sequence 14155, A
c	39	181	3.4	44120	3	US-09-949-016-14156	Sequence 14156, A
	40	181	3.4	265038	3	US-09-949-016-15779	Sequence 15779, A
	41	180.8	3.4	601	3	US-09-949-016-19567	Sequence 19567, A
	42	180.8	3.4	601	3	US-09-949-016-117194	Sequence 117194,
	43	180.6	3.4	66933	3	US-09-544-398B-11	Sequence 11, Appl
	44	180.6	3.4	66933	3	US-09-543-771B-11	Sequence 11, Appl
	45	180.6	3.4	72049	3	US-09-544-398B-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-306-828-34
; Sequence 34, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-34,

Query Match 100.0%; Score 5271; DB 3; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

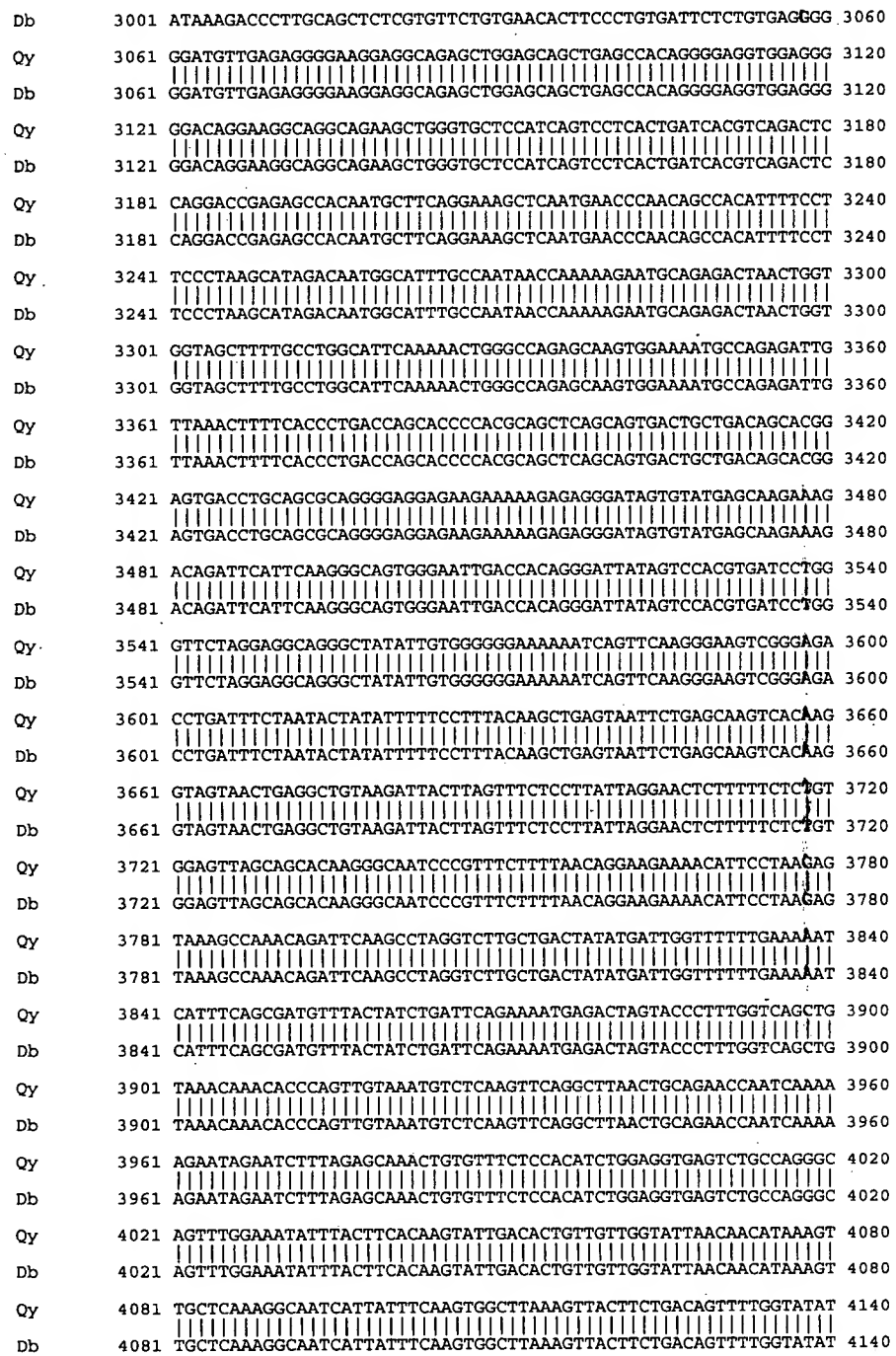
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
```


Db 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

```
Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy      3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db      3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy      3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db      3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy      4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db      4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy      4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db      4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Qy      4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db      4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Qy      4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db      4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Qy      4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db      4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy      4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db      4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy      4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db      4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy      4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db      4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy      4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Db      4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy      4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db      4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy      4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Db      4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy      4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
```

```
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271


RESULT 2
US-08-938-669A-3
; Sequence 3, Application US/08938669A
; Patent No. 6171788
;  GENERAL INFORMATION:
;    APPLICANT:  Nguyen, Thai D.
;    APPLICANT:  Polansky, Jon R.
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND
;    TITLE OF INVENTION:  RELATED DISEASES
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howrey & Simon
;      STREET:  1299 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004-2402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/938,669A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/791,154
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mendelson, Elliot
;      REGISTRATION NUMBER:  P-42,878
;      REFERENCE/DOCKET NUMBER:  07425-0034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 383-6857
;      TELEFAX:  202 383-6610
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6169 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-938-669A-3

  Query Match             100.0%;  Score 5271;  DB 3;  Length 6169;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
```

```
Qy       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
```

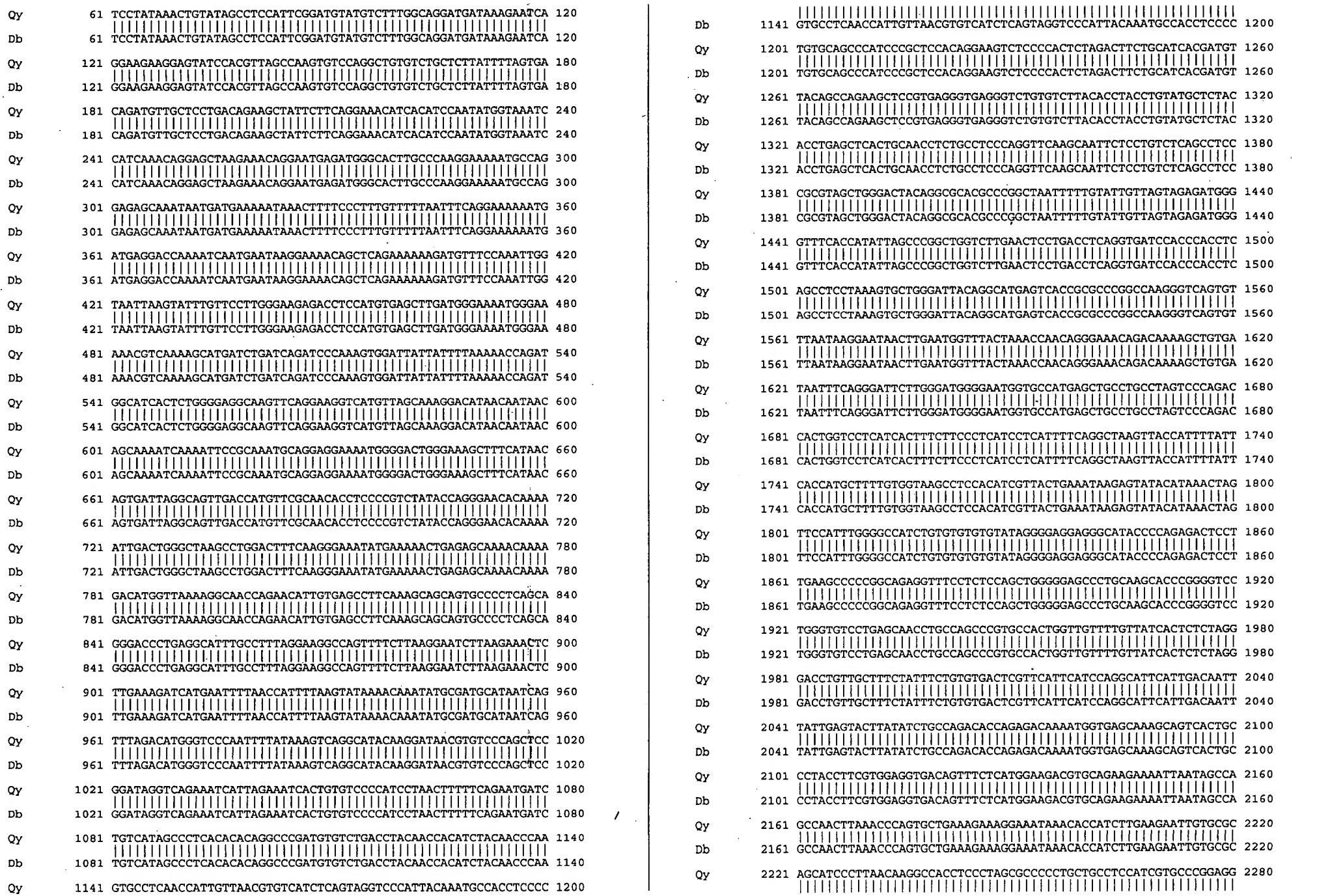

Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAACAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAACAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Qy 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Qy 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Db 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Qy 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Qy 4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Db 4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Qy 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Db 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Qy 4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Db 4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Qy 4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Db 4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Qy 4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Db 4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Qy 4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db 4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Qy 4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
Db 4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
Qy 5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
Db 5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
Qy 5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
Db 5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
Qy 5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
Db 5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

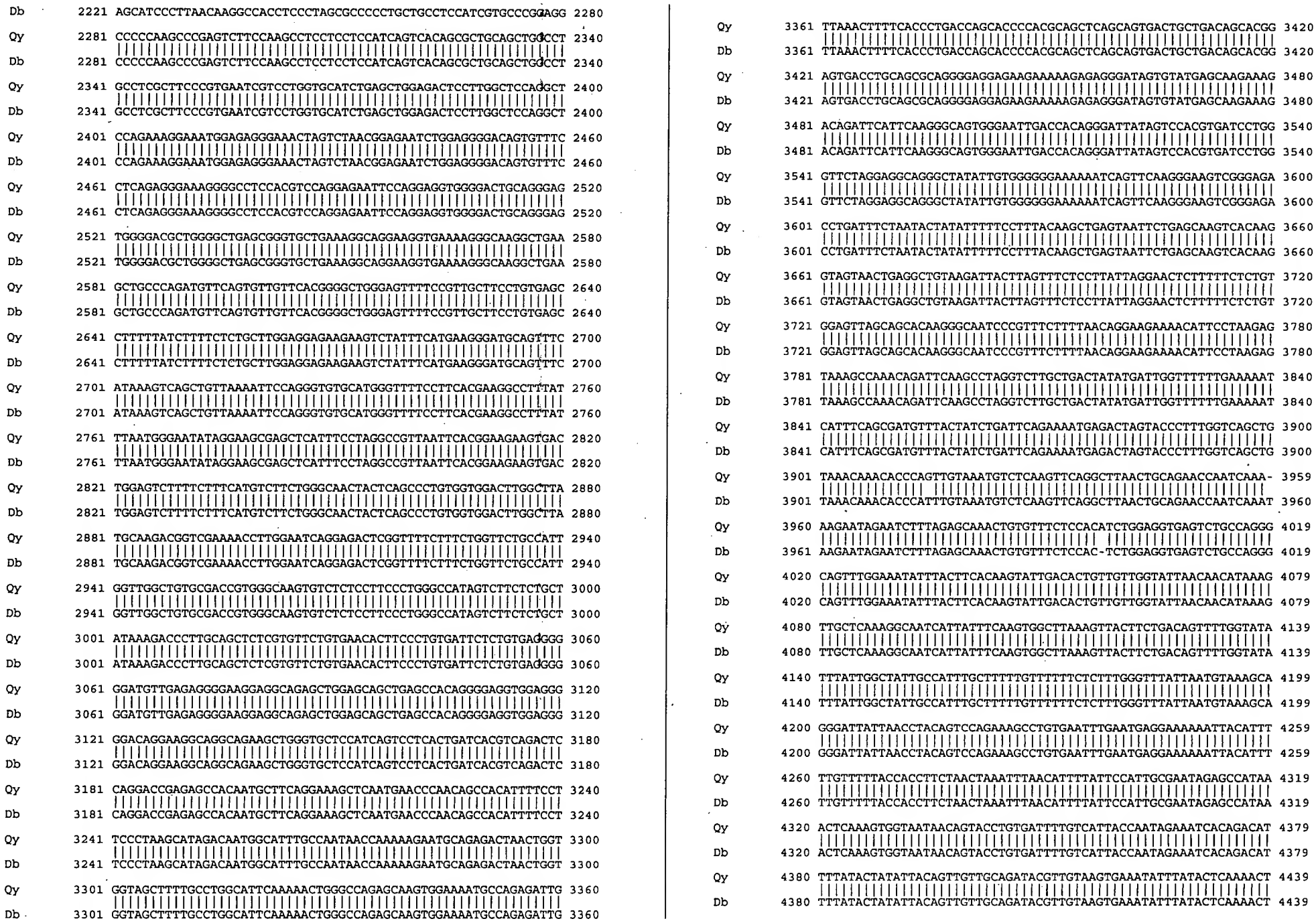
```
Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271


RESULT 3
US-09-306-828-3
; Sequence 3, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
;  APPLICANT: Nguyen, Thai D.
;  APPLICANT: Polansky, Jon R.
;  APPLICANT: Chen, Pu
;  APPLICANT: Chen, Hua
;  TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
;  CURRENT APPLICATION NUMBER: US/09/306,828
;  CURRENT FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/227,881
;  EARLIER FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
;   LENGTH: 6169
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-306-828-3

  Query Match             100.0%;  Score 5271;  DB 3;  Length 6169;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
```

```
Qy    1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db    1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy    1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db    1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy    1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db    1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy    1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db    1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy    1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db    1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy    2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db    2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy    2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db    2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy    2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db    2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy    2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db    2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy    2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db    2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy    2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db    2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy    2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db    2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy    2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGCAG 2520
Db    2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGCAG 2520

Qy    2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db    2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy    2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db    2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy    2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db    2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy    2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db    2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy    2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db    2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy    2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db    2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy    2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db    2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy    2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db    2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy    3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db    3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy    3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db    3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy    3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db    3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy    3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db    3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy    3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db    3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy    3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db    3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy    3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db    3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy    3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db    3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy    3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db    3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy    3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db    3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy    3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db    3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy    3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db    3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy    3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db    3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy    3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db    3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy    3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db    3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy    3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
```

```
Db       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

```
RESULT 4
US-08-938-669A-1
; Sequence 1, Application US/08938669A
; Patent No. 6171788
;  GENERAL INFORMATION:
;    APPLICANT:  Nguyen, Thai D.
;    APPLICANT:  Polansky, Jon R.
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND
;    TITLE OF INVENTION:  RELATED DISEASES
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howrey & Simon
;      STREET:  1299 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004-2402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/938,669A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/791,154
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mendelson, Elliot
;      REGISTRATION NUMBER:  P-42,878
;      REFERENCE/DOCKET NUMBER:  07425-0034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 383-6857
;      TELEFAX:  202 383-6610
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5300 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-938-669A-1

  Query Match            99.5%;  Score 5246.4;  DB 3;  Length 5300;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 5269;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
```


Qy 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Qy 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Db 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Qy 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Qy 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Qy 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280



```
Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

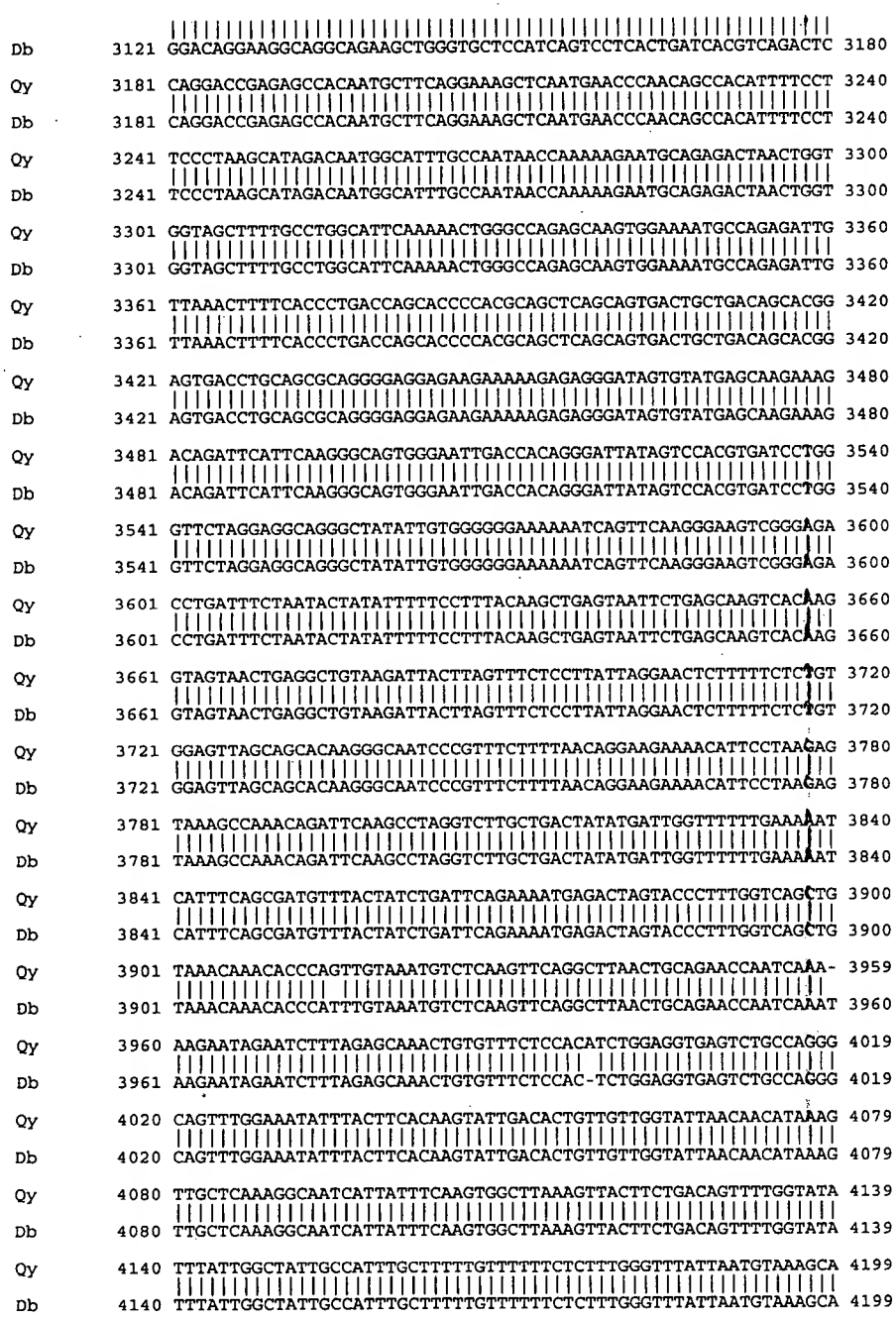
RESULT 5
US-09-306-828-1
; Sequence 1, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97

; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-1

Query Match 99.5%; Score 5246.4; DB 3; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

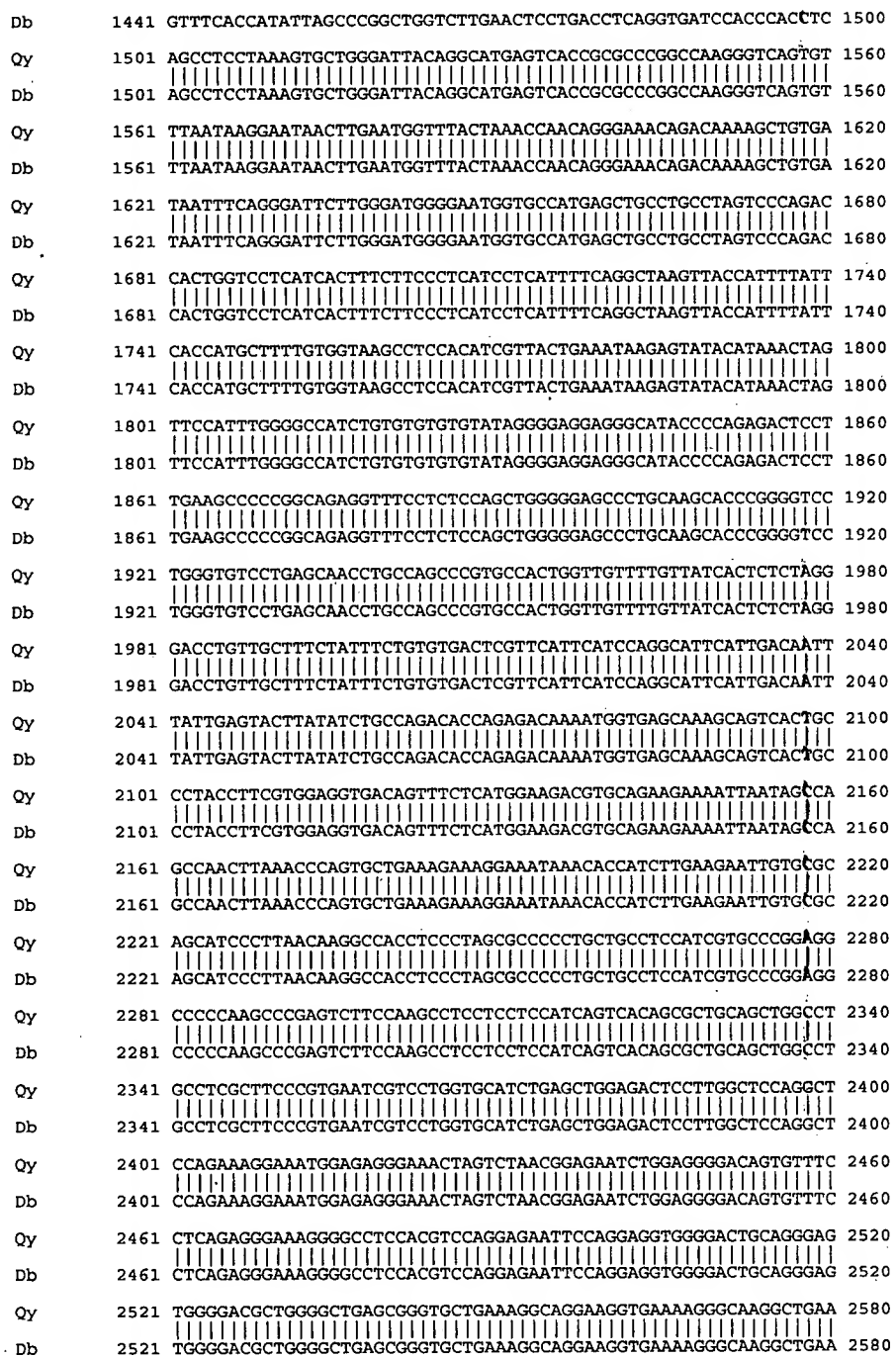
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
```

```
Qy       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
```



RESULT 6
US-08-938-669A-2

```
; Sequence 2, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
;   APPLICANT:  Nguyen, Thai D.
;   APPLICANT:  Polansky, Jon R.
;   TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;   TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND
;   TITLE OF INVENTION:  RELATED DISEASES
;   NUMBER OF SEQUENCES:  32
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Howrey & Simon
;     STREET:  1299 Pennsylvania Avenue, N.W.
;     CITY:  Washington
;     STATE:  DC
;     COUNTRY:  USA
;     ZIP:  20004-2402
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/938,669A
;     FILING DATE:
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/791,154
;     FILING DATE:  28-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Mendelson, Elliot
;     REGISTRATION NUMBER:  P-42,878
;     REFERENCE/DOCKET NUMBER:  07425-0034
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  202 383-6857
;     TELEFAX:  202 383-6610
;     TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  5304 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
US-08-938-669A-2

  Query Match             99.1%;  Score 5224.4;  DB 3;  Length 5304;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5264;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    3;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              |||.||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```


Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

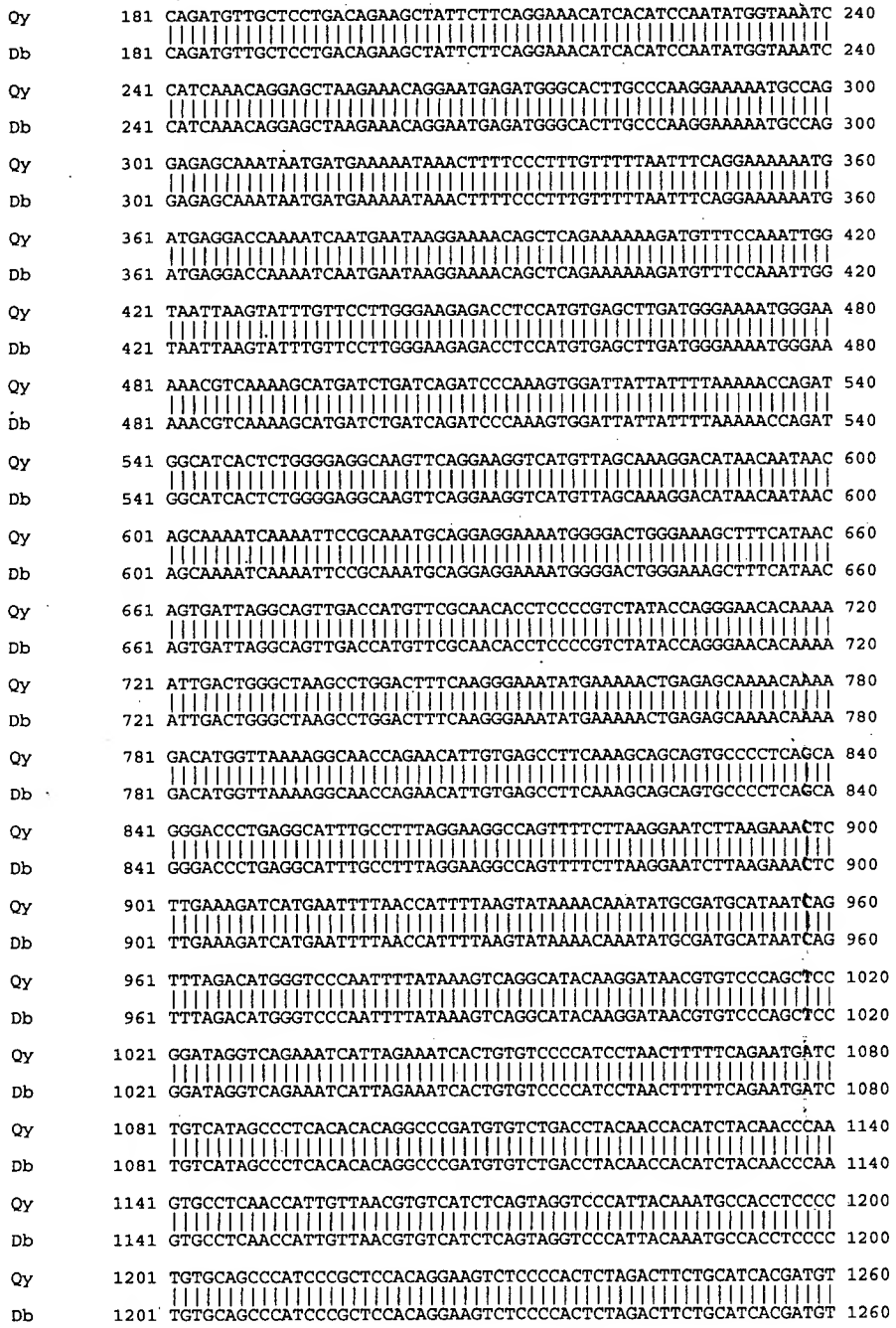
```
Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| 
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259

Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
```

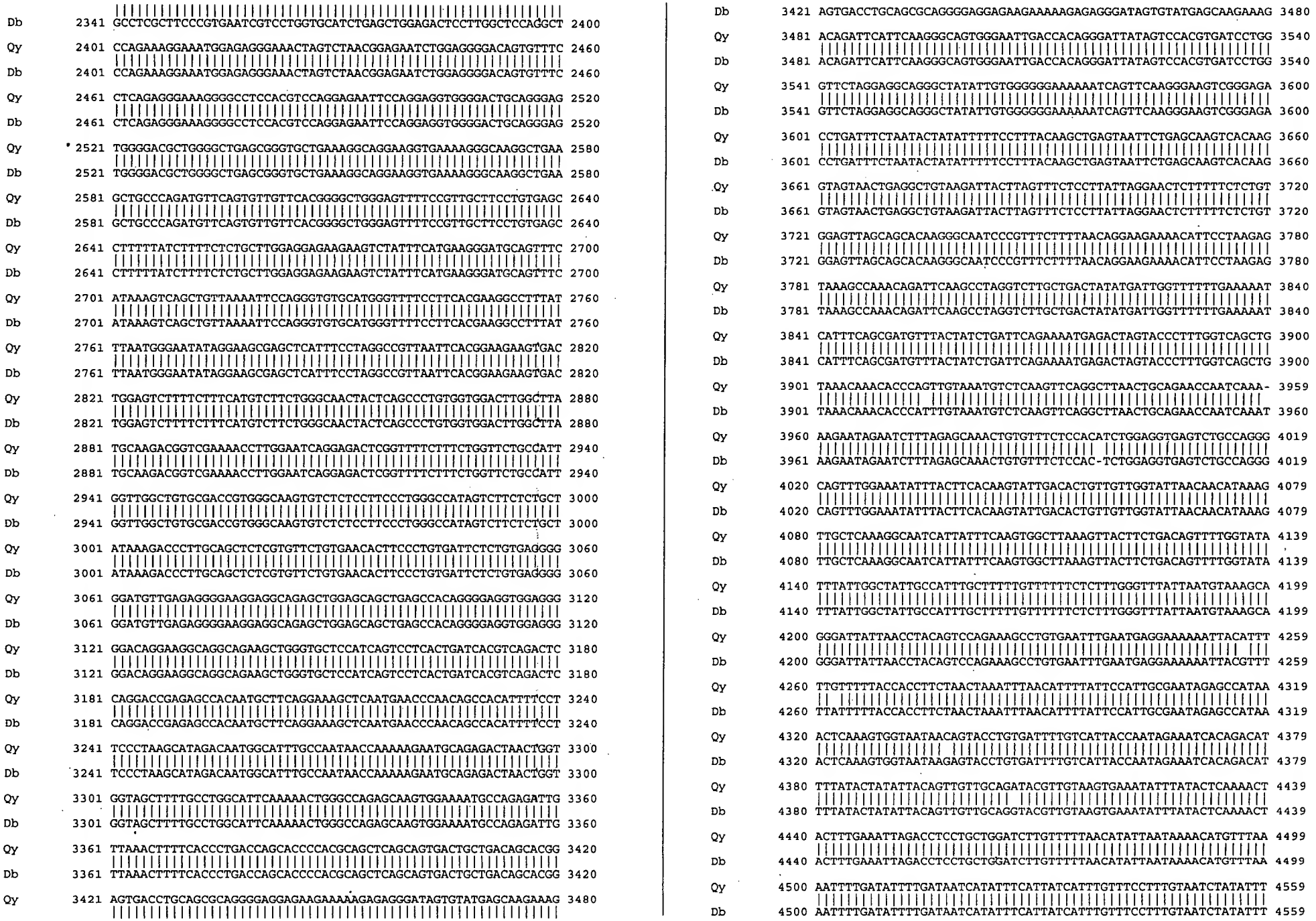
```
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
             ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy       5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099

Qy       5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159

Qy       5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219

Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
```

RESULT 7
US-09-306-828-2
; Sequence 2, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-2

Query Match 99.1%; Score 5224.4; DB 3; Length 5304;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
```


Qy 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Qy 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Qy 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400


Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259
Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db 4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db 4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db 4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

```
Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
             ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy       5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099

Qy       5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159

Qy       5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219

Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
```

```
RESULT 8
US-09-056-285A-1
; Sequence 1, Application US/09056285A
; Patent No. 6403307
;   GENERAL INFORMATION:
;       APPLICANT: Stone, Edwin M.
;                  Sheffield, Val C.
;                  Alward, Wallace L.M.
;                  Fingert, John
;       TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;       NUMBER OF SEQUENCES: 43
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: FOLEY, HOAG & ELIOT LLP
;            STREET: One Post Office Square
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109-2170
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/056,285A
;            FILING DATE: 07-Apr-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Arnold, Beth E.
;            REGISTRATION NUMBER: 35,430
;            REFERENCE/DOCKET NUMBER: UIA-010.28
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-832-1000
;            TELEFAX: 617-832-7000
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2800 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-056-285A-1

  Query Match           34.2%;  Score 1804.4;  DB 3;  Length 2800;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1838;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
```

```
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTTAC 4269

Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329

Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389

Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449

Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509

Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569

Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629

Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689

Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749

Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809

Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869

Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929

Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989

Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049

Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109

Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 5169

Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229

Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271

Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 9
US-10-017-870-10
; Sequence 10, Application US/10017870
; Patent No. 6727354
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/017,870
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-870-10

Query Match 34.2%; Score 1804.4; DB 3; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490

Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550

Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610

Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670

Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730

Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790

Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850

Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910

Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969

Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029

Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089

Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149

Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718
```

```
Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

```
             ||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 10
US-09-952-464A-1
; Sequence 1, Application US/09952464A
; Patent No. 6956103
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U11
; CURRENT APPLICATION NUMBER: US/09/952,464A
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; No. 6956103e =
; OTHER INFORMATION: Synthetic construct
US-09-952-464A-1

Query Match 34.2%; Score 1804.4; DB 3; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479
```

```
Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 11
US-09-306-828-38
; Sequence 38, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 38
; LENGTH: 227
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-38

Query Match 4.3%; Score 227; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.8e-46;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       5045 AACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 5104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 60

Qy       5105 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTG 5164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTG 120

Qy       5165 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTC 5224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTC 180

Qy       5225 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 227
```

RESULT 12
US-09-306-828-37
; Sequence 37, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua

```
;  TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
;  CURRENT APPLICATION NUMBER: US/09/306,828
;  CURRENT FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/227,881
;  EARLIER FILING DATE: 1999-01-11
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: Microsoft Word 97
; SEQ ID NO 37
;   LENGTH: 283
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-306-828-37

  Query Match             4.3%;  Score 227;  DB 3;  Length 283;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-46;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5045 AACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 5104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAA 60

Qy       5105 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTG 5164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTG 120

Qy       5165 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTC 5224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTC 180

Qy       5225 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 227


RESULT 13
US-09-949-016-15356/c
; Sequence 15356, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15356
;   LENGTH: 29326
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15356

  Query Match             3.6%;  Score 189.8;  DB 3;  Length 29326;
  Best Local Similarity   78.5%;  Pred. No. 7.4e-36;
  Matches  227;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || ||     ||| |  |  |  |  || |    |  | ||  ||||| |||||||
Db      23969 AGAGTCTCACTCTATTACCCAGGCTGAAGTGCAGTGGCGCAATCTCGGCTCATTGCAACC 23910

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             ||||||||||||||||||  ||||||||| || ||| |||||| ||||||||||||||||
Db      23909 TCTGCCTCCCAGGTTCAAGTGATTCTCCTGCCTTAGCTTCCCGAGTAGCTGGGACTACAG 23850

Qy       1400 GCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCG 1459
             || ||||||| |||||||||||||||| |||||| ||||||||||  || |||| ||| |
Db      23849 GCACACGCCCAGCTAATTTTTGTATTTTTAGTACAGATGGGGTTTTGCCGTATTGGCCAG 23790

Qy       1460 GCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGG 1519
             ||||||||  |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      23789 GCTGGTCTCAAACTCCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCTAAAGTGCTGGG 23730

Qy       1520 ATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAG 1568
             ||||||||  |||| |||| |||||||||  |      || || ||  ||
Db      23729 ATTACAGGTGTGAGCCACCACGCCCGGCCTGGAAAGGGTTTTAAAGTAG 23681


RESULT 14
US-09-949-016-15851/c
; Sequence 15851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15851
;   LENGTH: 205044
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(205044)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851

  Query Match             3.5%;  Score 184.6;  DB 3;  Length 205044;
  Best Local Similarity   78.0%;  Pred. No. 3.6e-34;
  Matches  238;  Conservative    0;  Mismatches   59;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || ||   | |||||  |  |  |     || |     |  || ||  ||||||||||||
Db     161178 AGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCACCATCTCGGCTCACTGCAACC 161119

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || ||||||| |||||||||||||||| |||||||||||| | ||||||||||||||||
Db     161118 TCCGCCTCCCGGGTTCAAGCAATTCTCCCGTCTCAGCCTCCTGAGTAGCTGGGACTACAG 161059

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
             |||         |||||||||||||||||||||| |||||| ||| ||| |||||||||
Db     161058 GCGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAAAGACGGGATTTCACCATG 160999

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
             || | | |||||||||||||||||||||||||||||||||||||||||| |||| |||||| |||
Db     160998 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAA 160939

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAA 1571
             |||||||||||||||||||||| ||||| ||| |||||||       |  ||  |||| |
Db     160938 GTGCTGGGATTACAGGCATGAGCCACCGTGCCTGGCCAAGACGTGATTATTTTTAAGAAT 160879

Qy       1572 TAACT 1576
              || |
Db     160878 AAAAT 160874


RESULT 15
US-09-949-016-15852/c
; Sequence 15852, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15852
;   LENGTH: 205044
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(205044)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852

  Query Match             3.5%;  Score 184.6;  DB 3;  Length 205044;
  Best Local Similarity   78.0%;  Pred. No. 3.6e-34;
  Matches  238;  Conservative    0;  Mismatches   59;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || ||   | |||||  |  |  |     || |    |  || ||  ||||||||||||
Db     161178 AGAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCACCATCTCGGCTCACTGCAACC 161119

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || ||||||| |||||||||||||||||| |||||||||||| | ||||||||||||||||
Db     161118 TCCGCCTCCCGGGTTCAAGCAATTCTCCCGTCTCAGCCTCCTGAGTAGCTGGGACTACAG 161059

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
              |||        |||||||||||||||||||||| |||||| ||| ||| |||||||||
Db     161058 GCGCCTGCCACCACGCCCGGCTAATTTTTGTATTTTTAGTAAAGACGGGATTTCACCATG 160999

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
              || | | ||||||||||||||||||||||||||||||||||| |||| |||||| |||
Db     160998 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCGCCTCGGCCTCCCAAA 160939

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAA 1571
              |||||||||||||||||||| ||||| ||| |||||||       |  ||  |||| |
Db     160938 GTGCTGGGATTACAGGCATGAGCCACCGTGCCTGGCCAAGACGTGATTATTTTTAAGAAT 160879

Qy       1572 TAACT 1576
              ||| |
Db     160878 AAAAT 160874


Search completed: January 26, 2006, 04:23:24
Job time : 614 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 26, 2006, 03:55:20 ; Search time 2551 Seconds
(without alignments)
17086.590 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagtttacctc.....tcgggcatgagccagcaagg 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	5271	100.0	5271	5	US-10-244-633-34	Sequence 34, Appl
	2	5271	100.0	6169	5	US-10-244-633-3	Sequence 3, Appli
	3	5246.4	99.5	5300	3	US-09-985-637A-1	Sequence 1, Appli
	4	5246.4	99.5	5300	5	US-10-244-633-1	Sequence 1, Appli
	5	5246.4	99.5	5300	7	US-10-741-339-1	Sequence 1, Appli
	6	5232.4	99.3	37252	5	US-10-087-192-1228	Sequence 1228, Ap
	7	5224.4	99.1	5304	5	US-10-244-633-2	Sequence 2, Appli
	8	4017.4	76.2	6000	9	US-10-509-595-1	Sequence 1, Appli
	9	1804.4	34.2	2800	3	US-09-952-464A-1	Sequence 1, Appli
	10	1804.4	34.2	2800	6	US-10-017-870-10	Sequence 10, Appl
	11	1804.4	34.2	2800	8	US-10-278-698-294	Sequence 294, App
	12	1804.4	34.2	2800	8	US-10-278-698-808	Sequence 808, App
	13	1804.4	34.2	2800	9	US-10-803-557-10	Sequence 10, Appl
	14	1804.4	34.2	2800	9	US-10-956-243-1	Sequence 1, Appli
	15	631.6	12.0	632	4	US-09-925-065A-905501	Sequence 905501,
c	16	629.6	11.9	630	4	US-09-925-065A-917000	Sequence 917000,
	17	546	10.4	571	4	US-09-925-065A-346049	Sequence 346049,
	18	394.6	7.5	545	4	US-09-925-065A-346051	Sequence 346051,
	19	394.4	7.5	1086	7	US-10-240-425-1586	Sequence 1586, Ap
	20	394.4	7.5	1086	8	US-10-723-860-927	Sequence 927, App
	21	394.4	7.5	1086	9	US-10-756-149-932	Sequence 932, App
	22	393	7.5	545	4	US-09-925-065A-346050	Sequence 346050,
c	23	284	5.4	296	8	US-10-674-124A-1442	Sequence 1442, Ap
c	24	284	5.4	296	8	US-10-674-124A-1443	Sequence 1443, Ap
	25	227	4.3	227	5	US-10-244-633-38	Sequence 38, Appl
	26	227	4.3	283	5	US-10-244-633-37	Sequence 37, Appl
	27	222.6	4.2	30057	5	US-10-087-192-1225	Sequence 1225, Ap
c	28	194.6	3.7	337344	8	US-10-388-838-58	Sequence 58, Appl
c	29	189.8	3.6	37443	8	US-10-719-993-6853	Sequence 6853, Ap
c	30	185.4	3.5	86361	7	US-10-741-601-5702	Sequence 5702, Ap
c	31	185.4	3.5	86361	8	US-10-741-600-17803	Sequence 17803, A
c	32	184.4	3.5	1744	6	US-10-104-047-1845	Sequence 1845, Ap
c	33	184.2	3.5	70779	5	US-10-087-192-1012	Sequence 1012, Ap
	34	183.2	3.5	41936	3	US-09-967-768A-116	Sequence 116, App
	35	183.2	3.5	41936	9	US-10-843-641A-6261	Sequence 6261, Ap
c	36	183.2	3.5	104245	6	US-10-160-807-4	Sequence 4, Appli
c	37	183.2	3.5	104245	7	US-10-655-847-4	Sequence 4, Appli
	38	183.2	3.5	170245	7	US-10-717-597-322	Sequence 322, App
c	39	182.2	3.5	5367	9	US-10-450-763-16437	Sequence 16437, A
	40	181.2	3.4	560	4	US-09-925-065A-127303	Sequence 127303,
c	41	181.2	3.4	196063	7	US-10-322-281-612	Sequence 612, App
	42	180.6	3.4	1620	4	US-09-925-065A-67041	Sequence 67041, A
	43	180.6	3.4	1620	4	US-09-925-065A-67042	Sequence 67042, A
	44	180.6	3.4	39725	6	US-10-017-161-1611	Sequence 1611, Ap
	45	180.6	3.4	39729	6	US-10-292-798-1285	Sequence 1285, Ap

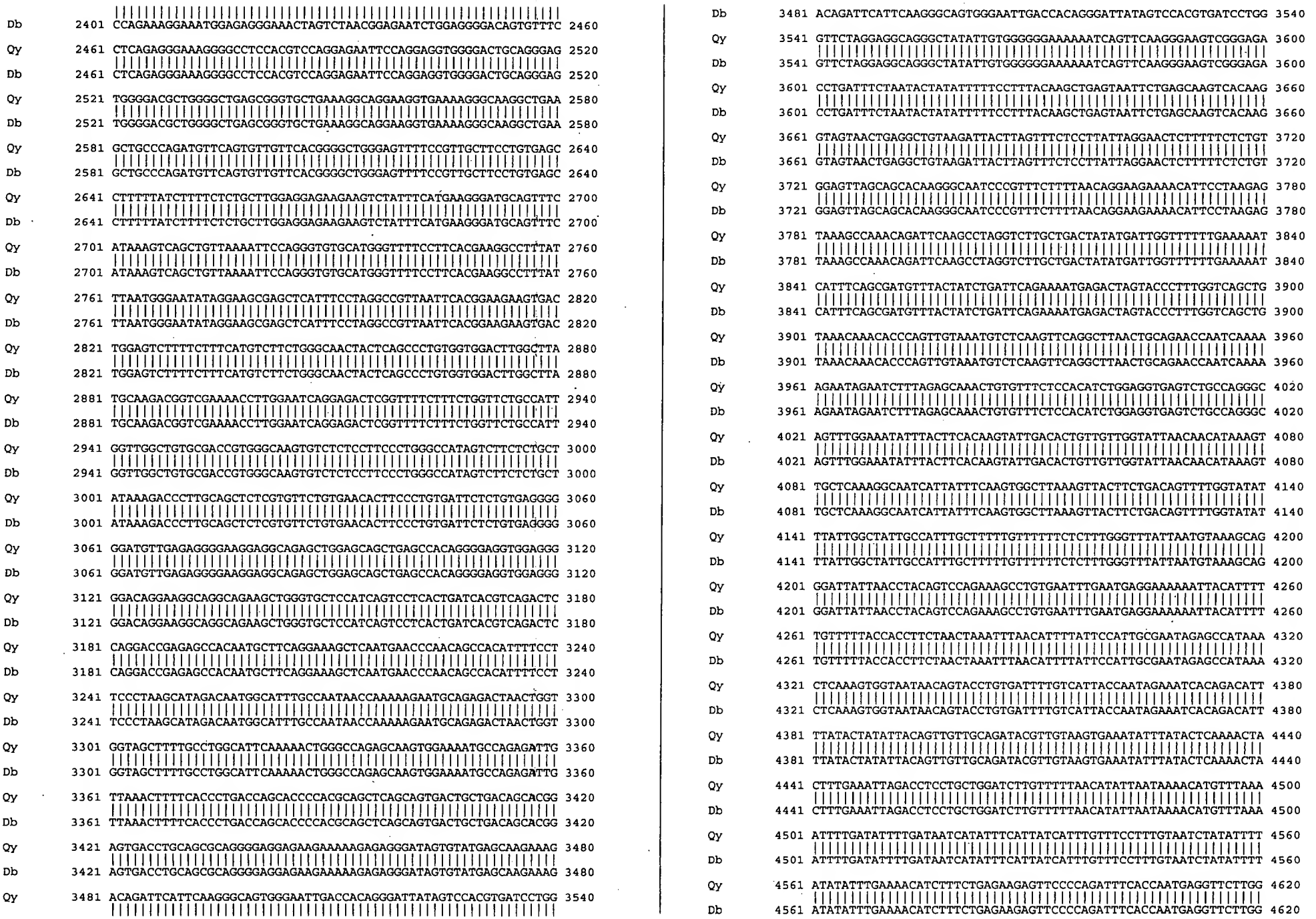
ALIGNMENTS

RESULT 1
US-10-244-633-34
; Sequence 34, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-34

Query Match 100.0%; Score 5271; DB 5; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
```

```
Qy       241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db       241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy       301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db       301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy       361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db       361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy       421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db       421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy       481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db       481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy       541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db       541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy       781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db       781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
```

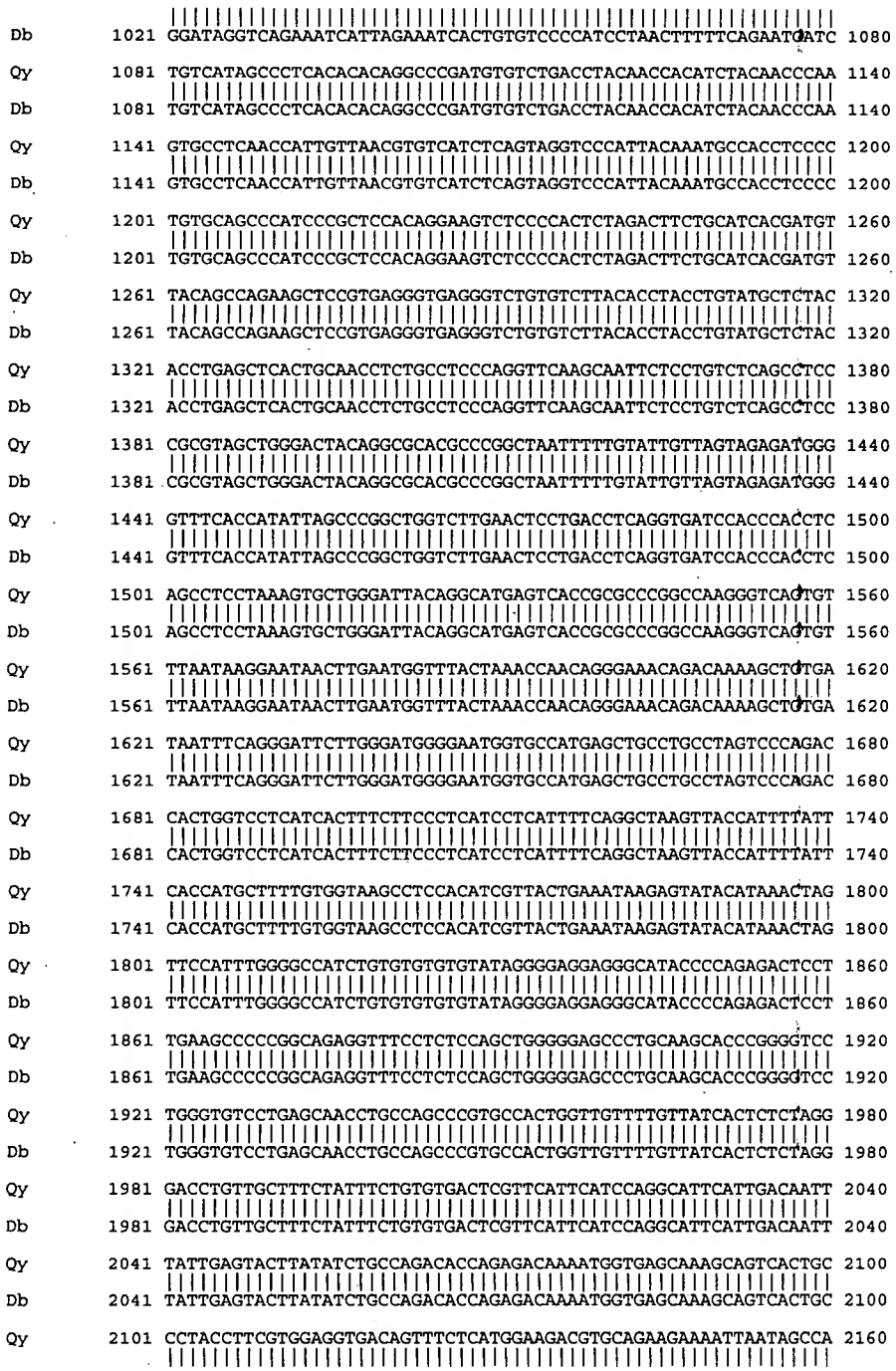

Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Qy 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
Qy 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Db 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Qy 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

```
Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 2
US-10-244-633-3
; Sequence 3, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
; LENGTH: 6169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-3

Query Match 100.0%; Score 5271; DB 5; Length 6169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
```


Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

```
Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Qy       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Qy       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Qy       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 3
US-09-985-637A-1
; Sequence 1, Application US/09985637A
; Publication No. US20030119000A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PI
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA

```
;  FILE REFERENCE: 13587.296
;  CURRENT APPLICATION NUMBER: US/09/985,637A
;  CURRENT FILING DATE:  2001-11-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 5300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-985-637A-1

  Query Match             99.5%;  Score 5246.4;  DB 3;  Length 5300;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5269;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
```

```
Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
```

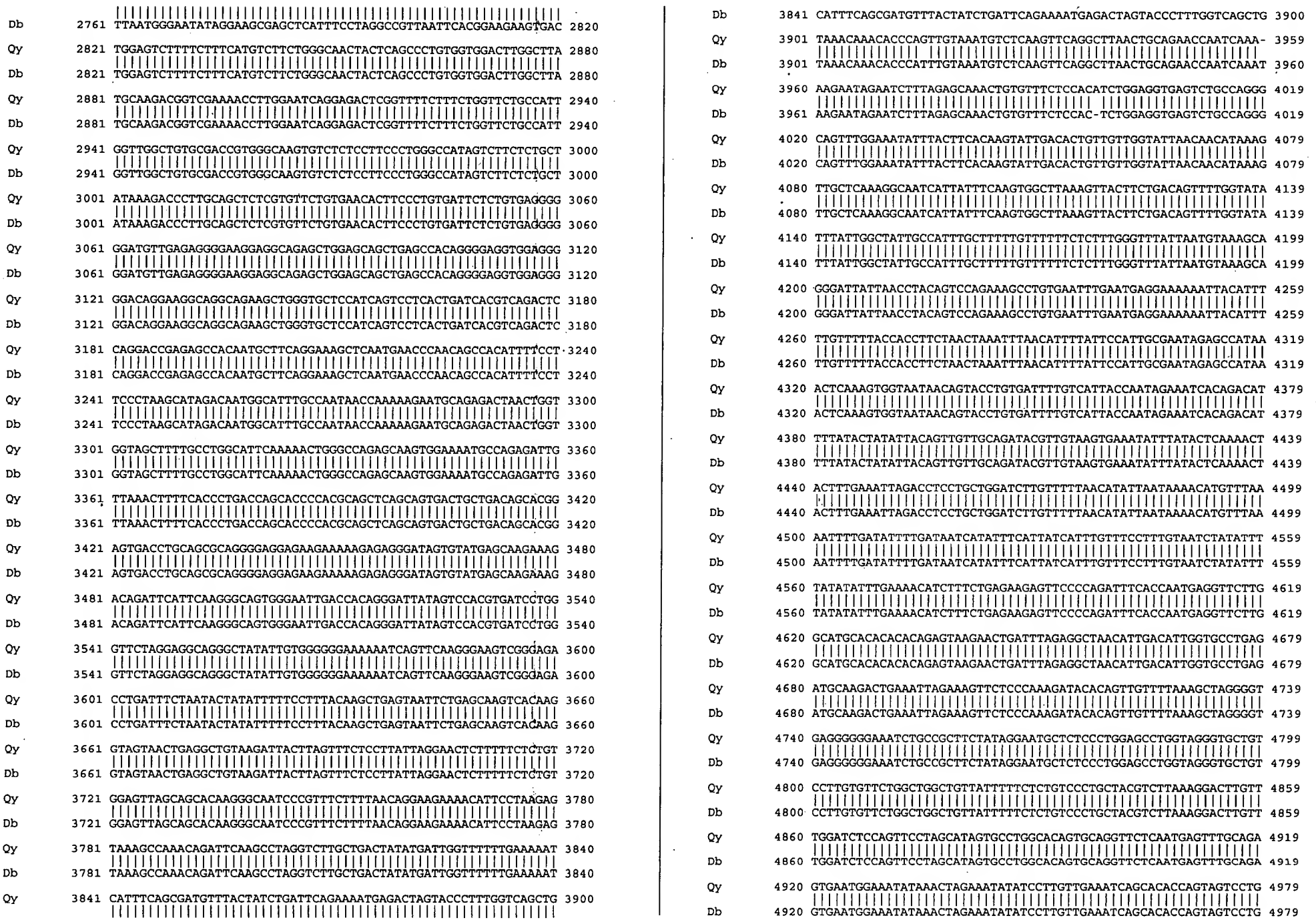
```
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259

Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTGCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 4
US-10-244-633-1
; Sequence 1, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-1

Query Match 99.5%; Score 5246.4; DB 5; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
```

```
Qy       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db       601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db       661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db       721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy       781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db       781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db       841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db       901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
```

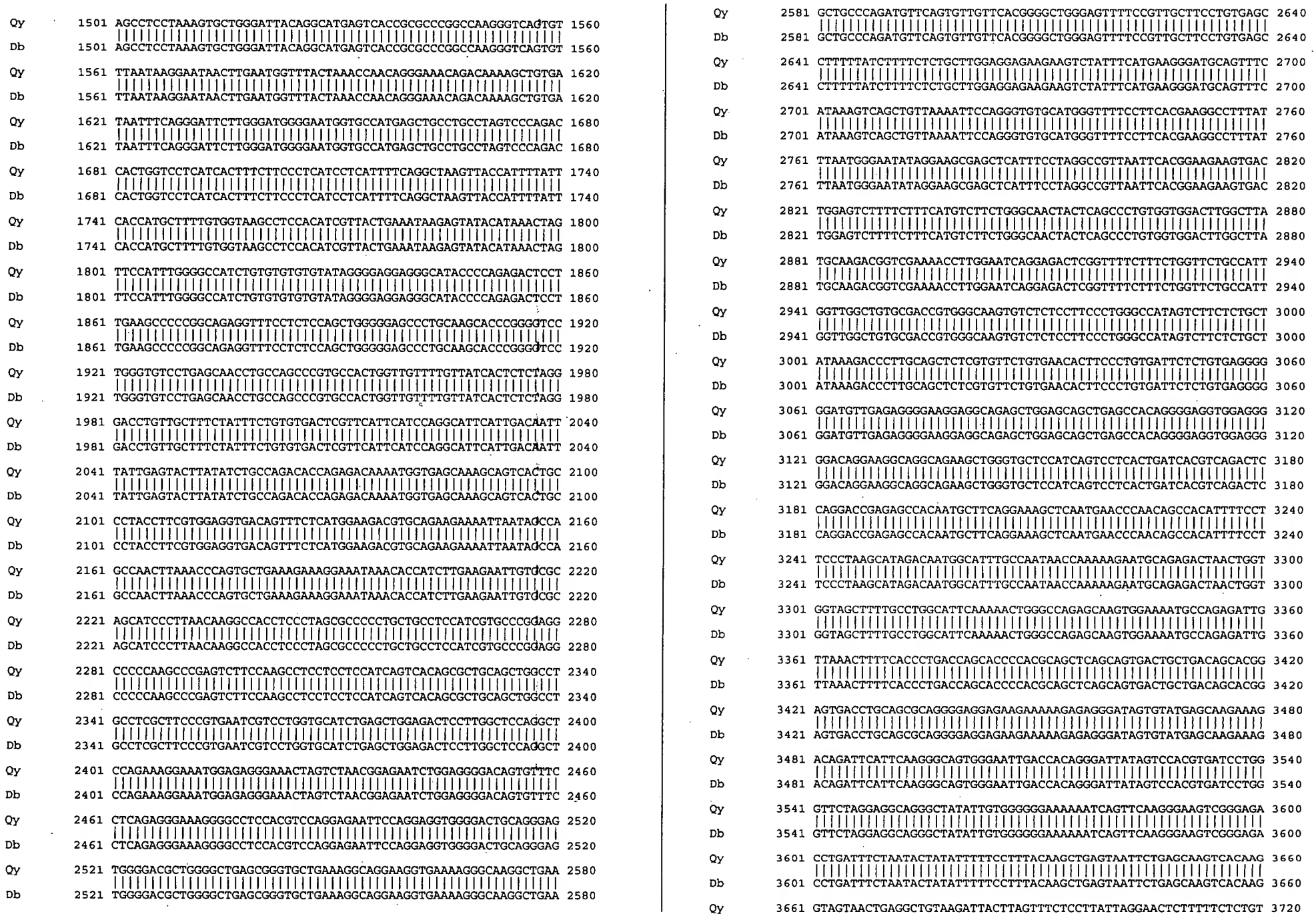

Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy 4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db 4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

```
Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 5
US-10-741-339-1
; Sequence 1, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PROP
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-339-1

Query Match 99.5%; Score 5246.4; DB 7; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
```

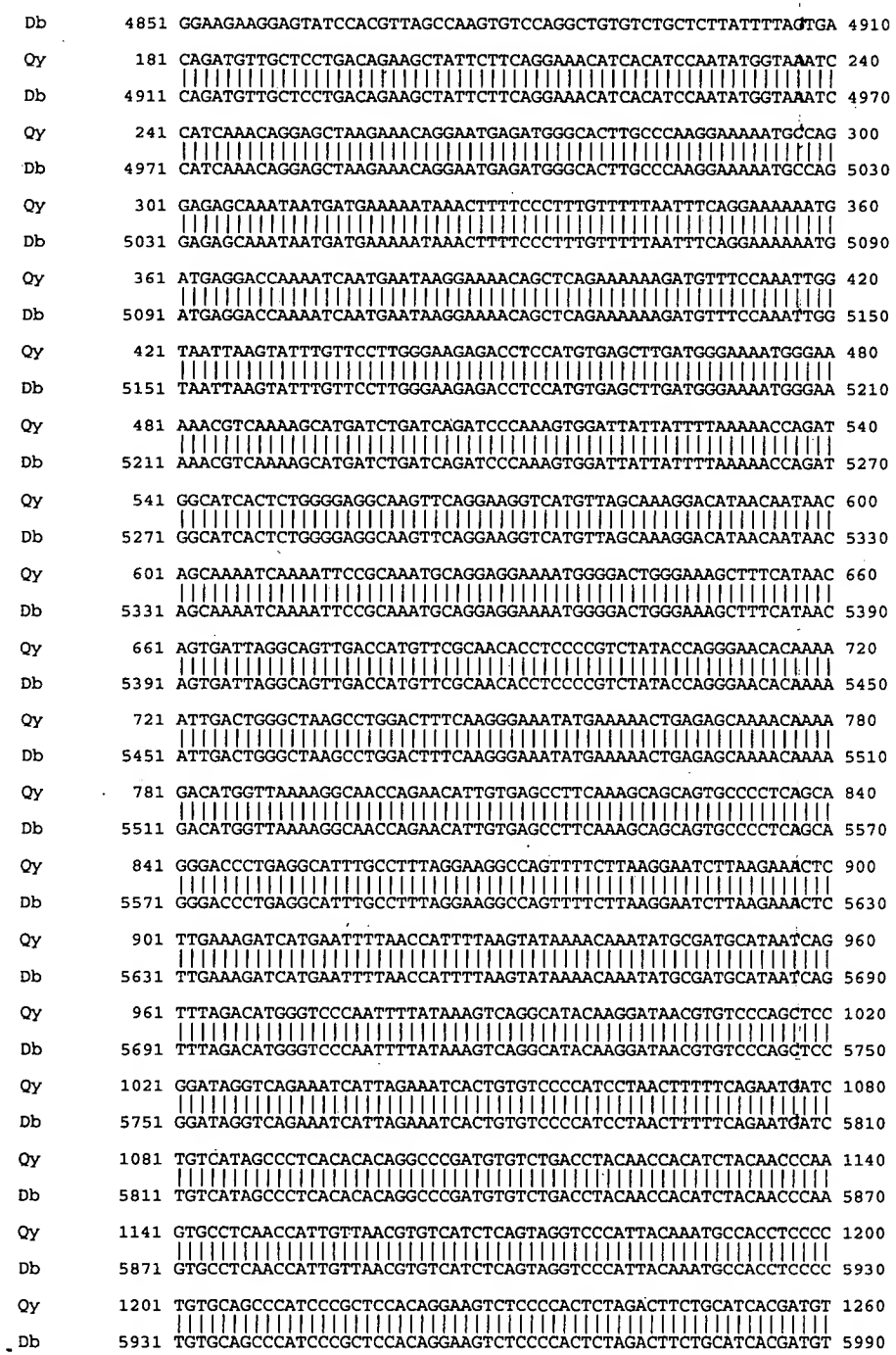

Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

```
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 6
US-10-087-192-1228
; Sequence 1228, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
; LENGTH: 37252
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-1228

Query Match 99.3%; Score 5232.4; DB 5; Length 37252;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5267; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Db       4731 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 4790
Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db       4791 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 4850
Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
```


Db 4851 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 4910
Qy 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db 4911 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 4970
Qy 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db 4971 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 5030
Qy 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db 5031 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 5090
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 5091 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 5150
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 5151 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 5210
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 5211 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 5270
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 5271 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 5330
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 5331 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 5390
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 5391 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 5450
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 5451 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 5510
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 5511 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 5570
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 5571 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 5630
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 5631 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 5690
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 5691 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGGTCC 5750
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 5751 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 5810
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 5811 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 5870
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 5871 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 5930
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 5931 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 5990
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 5991 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 6050
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 6051 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 6110
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 6111 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 6170
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 6171 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 6230
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 6231 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 6290
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 6291 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 6350
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 6351 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 6410
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 6411 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 6470
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 6471 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 6530
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 6531 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 6590
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 6591 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 6650
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 6651 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 6710
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 6711 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 6770
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 6771 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 6830
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 6831 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 6890
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 6891 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 6950
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 6951 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 7010
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 7011 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 7070

```
Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7071 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 7130

Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7131 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 7190

Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7191 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 7250

Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7251 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 7310

Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7311 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 7370

Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7371 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 7430

Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7431 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 7490

Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7491 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 7550

Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7551 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 7610

Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7611 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 7670

Qy       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7671 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 7730

Qy       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7731 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 7790

Qy       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7791 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 7850

Qy       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7851 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 7910

Qy       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7911 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 7970

Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7971 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 8030

Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8031 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 8090

Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8091 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 8150

Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8151 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 8210

Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8211 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 8270

Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8271 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 8330

Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8331 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 8390

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8391 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 8450

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8451 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 8510

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8511 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 8570

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8571 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 8630

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| 
Db       8631 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 8690

Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||| 
Db       8691 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 8749

Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8750 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 8809

Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8810 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 8869

Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8870 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 8929

Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8930 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 8989

Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8990 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 9049

Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9050 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 9109

Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9110 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 9169

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9170 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 9229

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       9230 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 9289

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9290 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 9349

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9350 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 9409

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9410 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 9469

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9470 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 9529

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9530 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 9589

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9590 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 9649

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9650 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 9709

Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       9710 GTGTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 9767

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9768 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 9827

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9828 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 9887

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9888 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 9947

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9948 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 9999
```

RESULT 7
US-10-244-633-2
; Sequence 2, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-2

Query Match 99.1%; Score 5224.4; DB 5; Length 5304;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
```

```
Qy       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259
Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db       4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db       4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db       4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy       4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039
Qy       5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
Db       5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099
Qy       5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
Db       5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159
Qy       5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219
Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
```

RESULT 8
US-10-509-595-1
; Sequence 1, Application US/10509595

; Publication No. US20050170353A1
; GENERAL INFORMATION:
; APPLICANT: Sysmex Corporation
; APPLICANT: ASANO, Kaoru
; APPLICANT: TAKAHATA, Takayuki
; APPLICANT: NUMADA, Shigehiro
; APPLICANT: MASAGO, Akinori
; APPLICANT: KOUCHI, Yasuhiro
; TITLE OF INVENTION: GENE EXAMINATION METHOD FOR JUDGING THE ONSET RISK OF GLAUCOMA
; FILE REFERENCE: Q83447
; CURRENT APPLICATION NUMBER: US/10/509,595
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-093443
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/JP03/03307
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 6000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-509-595-1

Query Match 76.2%; Score 4017.4; DB 9; Length 6000;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4052; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

```
Qy       1216 GCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGTTACAGCCAGAAGCTC 1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             1 GCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGTTACAGCCAGAAGCTC 60

Qy       1276 CGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC 1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            61 CGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGC 120

Qy       1336 AACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACT 1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           121 AACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACT 180

Qy       1396 ACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAG 1455
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           181 ACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAG 240

Qy       1456 CCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGC 1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           241 CCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGC 300

Qy       1516 TGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAAC 1575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           301 TGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAAC 360

Qy       1576 TTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGGGATTC 1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           361 TTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGGGATTC 420

Qy       1636 TTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCA 1695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           421 TTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCA 480

Qy       1696 CTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTG 1755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           481 CTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTG 540

Qy       1756 GTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAGTTCCATTTGGGGCCA 1815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           541 GTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAGTTCCATTTGGGGCCA 600

Qy       1816 TCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCAG 1875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           601 TCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCAG 660

Qy       1876 AGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCCTGGGTGTCCTGAGCA 1935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           661 AGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCCTGGGTGTCCTGAGCA 720

Qy       1936 ACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGGGACCTGTTGCTTTCT 1995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           721 ACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGGGACCTGTTGCTTTCT 780

Qy       1996 ATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATTTATTGAGTACTTATA 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           781 ATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATTTATTGAGTACTTATA 840

Qy       2056 TCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGCCCTACCTTCGTGGAG 2115
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           841 TCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGCCCTACCTTCGTGGAG 900

Qy       2116 GTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCAGCCAACTTAAACCCA 2175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           901 GTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCAGCCAACTTAAACCCA 960

Qy       2176 GTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGCAGCATCCCTTAACAA 2235
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           961 GTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGCAGCATCCCTTAACAA 1020

Qy       2236 GGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGGCCCCCAAGCCCGAGT 2295
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1021 GGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGGCCCCCAAGCCCGAGT 1080

Qy       2296 CTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCTGCCTCGCTTCCCGTG 2355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1081 CTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCTGCCTCGCTTCCCGTG 1140

Qy       2356 AATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCTCCAGAAAGGAAATGG 2415
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1141 AATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCTCCAGAAAGGAAATGG 1200

Qy       2416 AGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTCCTCAGAGGGAAAGGG 2475
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1201 AGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTCCTCAGAGGGAAAGGG 1260

Qy       2476 GCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAGTGGGGACGCTGGGGC 2535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1261 GCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAGTGGGGACGCTGGGGC 1320

Qy       2536 TGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAAGCTGCCCAGATGTTC 2595
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1321 TGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAAGCTGCCCAGATGTTC 1380

Qy       2596 AGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGCCTTTTTATCTTTTCT 2655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1381 AGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGCCTTTTTATCTTTTCT 1440

Qy       2656 CTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTCATAAAGTCAGCTGTT 2715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1441 CTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTCATAAAGTCAGCTGTT 1500

Qy       2716 AAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTATTTAATGGGAATATAG 2775
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1501 AAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTATTTAATGGGAATATAG 1560

Qy       2776 GAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGACTGGAGTCTTTTCTTT 2835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1561 GAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGACTGGAGTCTTTTCTTT 1620

Qy       2836 CATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTATGCAAGACGGTCGAA 2895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1621 CATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTATGCAAGACGGTCGAA 1680

Qy       2896 AACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATTGGTTGGCTGTGCGAC 2955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1681 AACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATTGGTTGGCTGTGCGAC 1740

Qy       2956 CGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCTATAAAGACCCTTGCA 3015
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1741 CGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCTATAAAGACCCTTGCA 1800
Qy       3016 GCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGGGGATGTTGAGAGGGG 3075
Db       1801 GCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGGGGATGTTGAGAGGGG 1860
Qy       3076 AAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGGGGACAGGAAGGCAGG 3135
Db       1861 AAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGGGGACAGGAAGGCAGG 1920
Qy       3136 CAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTCCAGGACCGAGAGCCA 3195
Db       1921 CAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTCCAGGACCGAGAGCCA 1980
Qy       3196 CAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCTTCCCTAAGCATAGAC 3255
Db       1981 CAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCTTCCCTAAGCATAGAC 2040
Qy       3256 AATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGTGGTAGCTTTTGCCTG 3315
Db       2041 AATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGTGGTAGCTTTTGCCTG 2100
Qy       3316 GCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTGTTAAACTTTTCACCC 3375
Db       2101 GCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTGTTAAACTTTTCACCC 2160
Qy       3376 TGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGGAGTGACCTGCAGCGC 3435
Db       2161 TGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGGAGTGACCTGCAGCGC 2220
Qy       3436 AGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 3495
Db       2221 AGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCATTCAAG 2280
Qy       3496 GGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAGGCAGG 3555
Db       2281 GGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAGGCAGG 2340
Qy       3556 GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCTAATAC 3615
Db       2341 GCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCTAATAC 2400
Qy       3616 TATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTGAGGCT 3675
Db       2401 TATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTGAGGCT 2460
Qy       3676 GTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCAGCACA 3735
Db       2461 GTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCAGCACA 2520
Qy       3736 AGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAACAGAT 3795
Db       2521 AGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAACAGAT 2580
Qy       3796 TCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCGATGTT 3855
Db       2581 TCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCGATGTT 2640
Qy       3856 TACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACACCCAG 3915
Db       2641 TACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACACCCAT 2700
Qy       3916 TTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAATCTTT 3974
Db       2701 TTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAATCTTT 2760
Qy       3975 AGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAAATATT 4034
Db       2761 AGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAAATATT 2819
Qy       4035 TACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAGGCAAT 4094
Db       2820 TACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAGGCAAT 2879

Qy       4095 CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCTATTGC 4154
Db       2880 CATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCTATTGC 2939
Qy       4155 CATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTAACCTA 4214
Db       2940 CATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTAACCTA 2999
Qy       4215 CAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTACCACCT 4274
Db       3000 CAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTACCACCT 3059
Qy       4275 TCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTGGTAAT 4334
Db       3060 TCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTGGTAAT 3119
Qy       4335 AACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTATATTAC 4394
Db       3120 AACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTATATTAC 3179
Qy       4395 AGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAATTAGAC 4454
Db       3180 AGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAATTAGAC 3239
Qy       4455 CTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATATTTTG 4514
Db       3240 CTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATATTTTG 3299
Qy       4515 ATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTGAAAAC 4574
Db       3300 ATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTGAAAAC 3359
Qy       4575 ATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACACACACA 4634
Db       3360 ATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACACACACA 3419
Qy       4635 GAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACTGAAAT 4694
Db       3420 GAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACTGAAAT 3479
Qy       4695 TAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAAATCTG 4754
Db       3480 TAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAAATCTG 3539
Qy       4755 CCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTCTGGCT 4814
Db       3540 CCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTCTGGCT 3599
Qy       4815 GGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCAGTTCC 4874
Db       3600 GGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCAGTTCC 3659
Qy       4875 TAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAAATATA 4934
Db       3660 TAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAAATATA 3719
Qy       4935 AACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTGTGTA 4994
Db       3720 AACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGTGTGTA 3779
Qy       4995 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTATTATT 5054
Db       3780 C--GTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTATTATT 3837
Qy       5055 GGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGACTTCTG 5114
Db       3838 GGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGACTTCTG 3897
Qy       5115 GAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCACAGCCC 5174
Db       3898 GAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCACAGCCC 3957
```

```
Qy       5175 CACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAGTATAT 5234
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3958 CACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAGTATAT 4017

Qy       5235 ATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||
Db       4018 ATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 4054


RESULT 9
US-09-952-464A-1
; Sequence 1, Application US/09952464A
; Publication No. US20030077587A1
; GENERAL INFORMATION:
;  APPLICANT: Stone, Edwin M.
;  APPLICANT:  Sheffield, Val C.
;  APPLICANT:  Alward, Wallace L.M.
;  APPLICANT:  Fingert, John
;  TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;  FILE REFERENCE: 21087.0017U11
;  CURRENT APPLICATION NUMBER: US/09/952,464A
;  CURRENT FILING DATE:  2001-09-12
;  PRIOR APPLICATION NUMBER: 09/473,273
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 09/461,542
;  PRIOR FILING DATE: 1999-12-15
;  PRIOR APPLICATION NUMBER: 09/366,952
;  PRIOR FILING DATE: 1999-08-04
;  PRIOR APPLICATION NUMBER: 09/056,285
;  PRIOR FILING DATE: 1998-04-07
;  PRIOR APPLICATION NUMBER: 08/822,999
;  PRIOR FILING DATE: 1997-03-21
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2800
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587A1e =
;   OTHER INFORMATION: Synthetic construct
US-09-952-464A-1

  Query Match            34.2%;  Score 1804.4;  DB 3;  Length 2800;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1838;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498
```

```
Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 10
US-10-017-870-10
; Sequence 10, Application US/10017870
; Publication No. US20030165857A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/017,870
; CURRENT FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-870-10

Query Match 34.2%; Score 1804.4; DB 6; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840


RESULT 11
US-10-278-698-294
; Sequence 294, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
;  APPLICANT: PathoArray GmbH
;  APPLICANT:  Stuhlmuller, Bruno
;  APPLICANT:  Haupl, Thomas
;  TITLE OF INVENTION: Nucleic Acid Array
;  FILE REFERENCE: O30027US
;  CURRENT APPLICATION NUMBER: US/10/278,698
;  CURRENT FILING DATE:  2002-10-23
;  NUMBER OF SEQ ID NOS: 1050
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 294
;   LENGTH: 2800
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-278-698-294

  Query Match             34.2%;  Score 1804.4;  DB 8;  Length 2800;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1838;  Conservative    0;  Mismatches    1;  Indels    3;  Gaps    3;

Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438
```

```
Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 12
US-10-278-698-808
; Sequence 808, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmuller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 808
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-808

Query Match 34.2%; Score 1804.4; DB 8; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| |||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db         480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db         540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378
```

```
Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 13
US-10-803-557-10
; Sequence 10, Application US/10803557
; Publication No. US20050095609A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, DOUG HUI
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS
; FILE REFERENCE: 034827-1401
; CURRENT APPLICATION NUMBER: US/10/803,557
; CURRENT FILING DATE: 2004-03-17
; PRIOR APPLICATION NUMBER: US/10/017,870
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-557-10

Query Match 34.2%; Score 1804.4; DB 9; Length 2800;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239
```

```
Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969
             |||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
```

```
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869

Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929

Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989

Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049

Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109

Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTCCAC 5169

Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTCCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229

Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271

Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

RESULT 14
US-10-956-243-1
; Sequence 1, Application US/10956243
; Publication No. US20050123960A1
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Alward, Wallace L.M.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U11
; CURRENT APPLICATION NUMBER: US/10/956,243
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US/09/952,464
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: Synthetic construct
US-10-956-243-1

Query Match 34.2%; Score 1804.4; DB 9; Length 2800;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1838; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

```
Qy       3431 AGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 3490

Db          1 AGCGCAGGGGAGGAGAAG-AAAAGAGAGGGATAGTGTATGAGCAAGAAAGACAGATTCAT 59

Qy       3491 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 3550

Db         60 TCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGGGTTCTAGGAG 119

Qy       3551 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 3610

Db        120 GCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGACCTGATTTCT 179

Qy       3611 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 3670

Db        180 AATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAGGTAGTAACTG 239

Qy       3671 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 3730

Db        240 AGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGTGGAGTTAGCA 299

Qy       3731 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 3790

Db        300 GCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAGTAAAGCCAAA 359

Qy       3791 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 3850

Db        360 CAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAATCATTTCAGCG 419

Qy       3851 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 3910

Db        420 ATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTGTAAACAAACA 479

Qy       3911 CCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA-AAGAATAGAA 3969

Db        480 CCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAATAAGAATAGAA 539

Qy       3970 TCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 4029

Db        540 TCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGGCAGTTTGGAA 598

Qy       4030 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 4089

Db        599 ATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGTTGCTCAAAG 658

Qy       4090 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 4149

Db        659 GCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATATTTATTGGCT 718

Qy       4150 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 4209

Db        719 ATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAGGGATTATTA 778

Qy       4210 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 4269

Db        779 ACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTTTGTTTTTAC 838

Qy       4270 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 4329

Db        839 CACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAACTCAAAGTG 898

Qy       4330 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 4389

Db        899 GTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATTTTATACTAT 958

Qy       4390 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 4449

Db        959 ATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTACTTTGAAAT 1018

Qy       4450 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 4509
```

```
Db       1019 TAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAAATTTTGATA 1078

Qy       4510 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 4569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 TTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTTATATATTTG 1138

Qy       4570 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 4629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 AAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGGCATGCACAC 1198

Qy       4630 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 4689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGATGCAAGACT 1258

Qy       4690 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 4749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 GAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTGAGGGGGGAA 1318

Qy       4750 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 4809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 ATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTCCTTGTGTTC 1378

Qy       4810 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 4869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 TGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTTGGATCTCCA 1438

Qy       4870 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 4929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1439 GTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAGTGAATGGAA 1498

Qy       4930 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 4989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1499 ATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGGTGTAAGTGT 1558

Qy       4990 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 5049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 GTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATATAGGAACTA 1618

Qy       5050 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 5109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1619 TTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTCCAAACAGAC 1678

Qy       5110 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCCTGTGCAC 5169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1679 TTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCCCCTGTGCAC 1738

Qy       5170 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 5229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1739 AGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTGGCTCCCCAG 1798

Qy       5230 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||
Db       1799 TATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 1840
```

```
RESULT 15
US-09-925-065A-905501
; Sequence 905501, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 905501
;   LENGTH: 632
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-905501

  Query Match             12.0%;  Score 631.6;  DB 4;  Length 632;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-145;
  Matches  631;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1284 TGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTG 1343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTG 60

Qy       1344 CCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCGC 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCGC 120

Qy       1404 ACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGCTG 1463
             |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ACGCCMGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGCTG 180

Qy       1464 GTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGATTA 1523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGATTA 240

Qy       1524 CAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGAATGG 1583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGAATGG 300

Qy       1584 TTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGGGATTCTTGGGATG 1643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 TTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGGGATTCTTGGGATG 360

Qy       1644 GGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCACTTTCTTC 1703
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGACCACTGGTCCTCATCACTTTCTTC 420

Qy       1704 CCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTGGTAAGCCT 1763
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATTCACCATGCTTTTGTGGTAAGCCT 480

Qy       1764 CCACATCGTTACTGAAATAAGAGTATACATAAACTAGTTCCATTTGGGGCCATCTGTGTG 1823
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CCACATCGTTACTGAAATAAGAGTATACATAAACTAGTTCCATTTGGGGCCATCTGTGTG 540

Qy       1824 TGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCAGAGGTTTCC 1883
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCTTGAAGCCCCCGGCAGAGGTTTCC 600

Qy       1884 TCTCCAGCTGGGGGAGCCCTGCAAGCACCCGG 1915
             ||||||||||||||||||||||||||||||||
Db         601 TCTCCAGCTGGGGGAGCCCTGCAAGCACCCGG 632

Search completed: January 26, 2006, 10:09:05
Job time : 2632 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 26, 2006, 04:13:16 ; Search time 514 Seconds
(without alignments)
8518.386 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagtttacctc.....tcgggcatgagccagcaagg 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

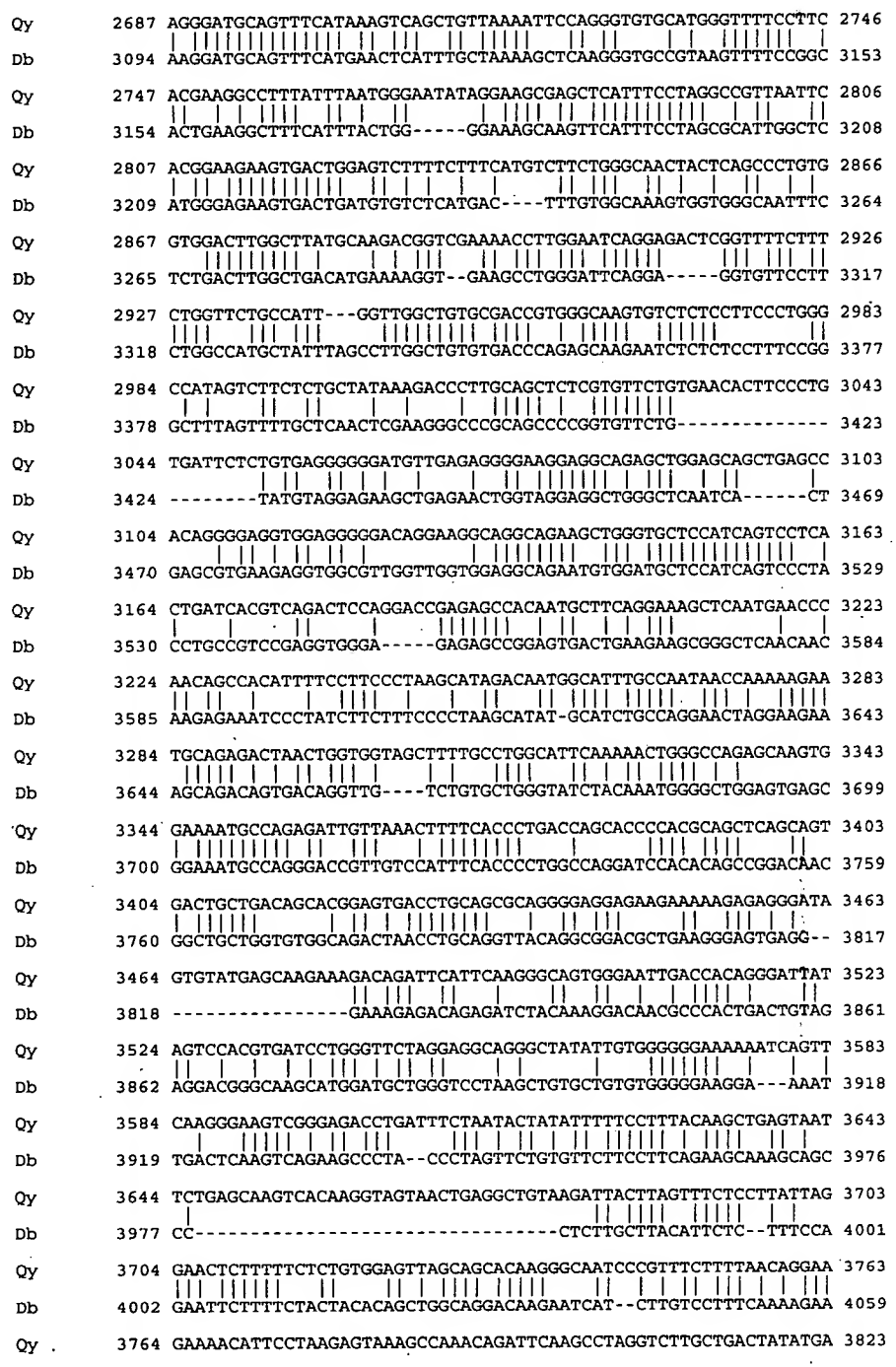
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	190.8	3.6	16525	8	US-11-136-527-717	Sequence 717, App
c	2	185.4	3.5	86361	7	US-10-995-561-13364	Sequence 13364, A
	3	185.2	3.5	143389	8	US-11-112-908-30	Sequence 30, Appl
	4	185.2	3.5	150314	8	US-11-112-908-24	Sequence 24, Appl
	5	185.2	3.5	166020	8	US-11-112-908-28	Sequence 28, Appl
c	6	184	3.5	60754	7	US-10-995-561-13440	Sequence 13440, A
	7	183.4	3.5	415117	7	US-10-995-561-13274	Sequence 13274, A
	8	179.6	3.4	14804	7	US-10-995-561-13379	Sequence 13379, A
c	9	179.6	3.4	98716	7	US-10-995-561-13331	Sequence 13331, A
	10	179.6	3.4	191091	8	US-11-121-086-60	Sequence 60, Appl
c	11	179	3.4	159497	8	US-11-112-908-61	Sequence 61, Appl
c	12	179	3.4	171427	8	US-11-112-908-60	Sequence 60, Appl
c	13	178.4	3.4	127917	7	US-10-775-169-82	Sequence 82, Appl
	14	177.8	3.4	161994	8	US-11-112-908-57	Sequence 57, Appl
	15	177.8	3.4	168656	8	US-11-112-908-59	Sequence 59, Appl
	16	177.8	3.4	170285	8	US-11-112-908-58	Sequence 58, Appl
c	17	177.8	3.4	387780	7	US-10-995-561-13259	Sequence 13259, A
	18	177.6	3.4	128978	7	US-10-775-169-345	Sequence 345, App
c	19	176.8	3.4	53332	7	US-10-786-065-3	Sequence 3, Appli
	20	176.8	3.4	179777	8	US-11-121-086-106	Sequence 106, App
c	21	176.6	3.4	1154	8	US-11-145-703-37	Sequence 37, Appl
	22	176.6	3.4	153142	8	US-11-121-086-27	Sequence 27, Appl
c	23	176.2	3.3	1301	8	US-11-145-703-36	Sequence 36, Appl
c	24	176.2	3.3	1386	8	US-11-145-703-40	Sequence 40, Appl
	25	176	3.3	207600	8	US-11-112-908-31	Sequence 31, Appl
c	26	176	3.3	319608	8	US-11-145-703-1	Sequence 1, Appli
	27	175.6	3.3	177623	8	US-11-112-908-41	Sequence 41, Appl
	28	175	3.3	86081	7	US-10-995-561-13246	Sequence 13246, A
c	29	174.8	3.3	17455	7	US-10-995-561-13426	Sequence 13426, A
c	30	174.8	3.3	28724	7	US-10-995-561-13372	Sequence 13372, A
c	31	174.8	3.3	155989	8	US-11-121-086-57	Sequence 57, Appl
c	32	174.8	3.3	180654	8	US-11-121-086-58	Sequence 58, Appl
c	33	174.6	3.3	40987	7	US-10-995-561-13503	Sequence 13503, A
	34	174.6	3.3	67088	7	US-10-995-561-13365	Sequence 13365, A
c	35	174.6	3.3	79528	7	US-10-276-233A-6	Sequence 6, Appli
	36	174.4	3.3	60844	7	US-10-995-561-13359	Sequence 13359, A
c	37	174.2	3.3	115935	7	US-10-775-169-241	Sequence 241, App
c	38	174.2	3.3	141121	7	US-10-995-561-13262	Sequence 13262, A
c	39	174.2	3.3	162289	8	US-11-121-086-20	Sequence 20, Appl
c	40	174.2	3.3	191684	8	US-11-121-086-2	Sequence 2, Appli
	41	174.2	3.3	197096	8	US-11-121-086-107	Sequence 107, App
c	42	174	3.3	13609	7	US-10-995-561-13442	Sequence 13442, A
c	43	174	3.3	16082	7	US-10-995-561-13485	Sequence 13485, A
c	44	174	3.3	23894	7	US-10-995-561-13320	Sequence 13320, A
	45	174	3.3	87672	7	US-10-995-561-13237	Sequence 13237, A

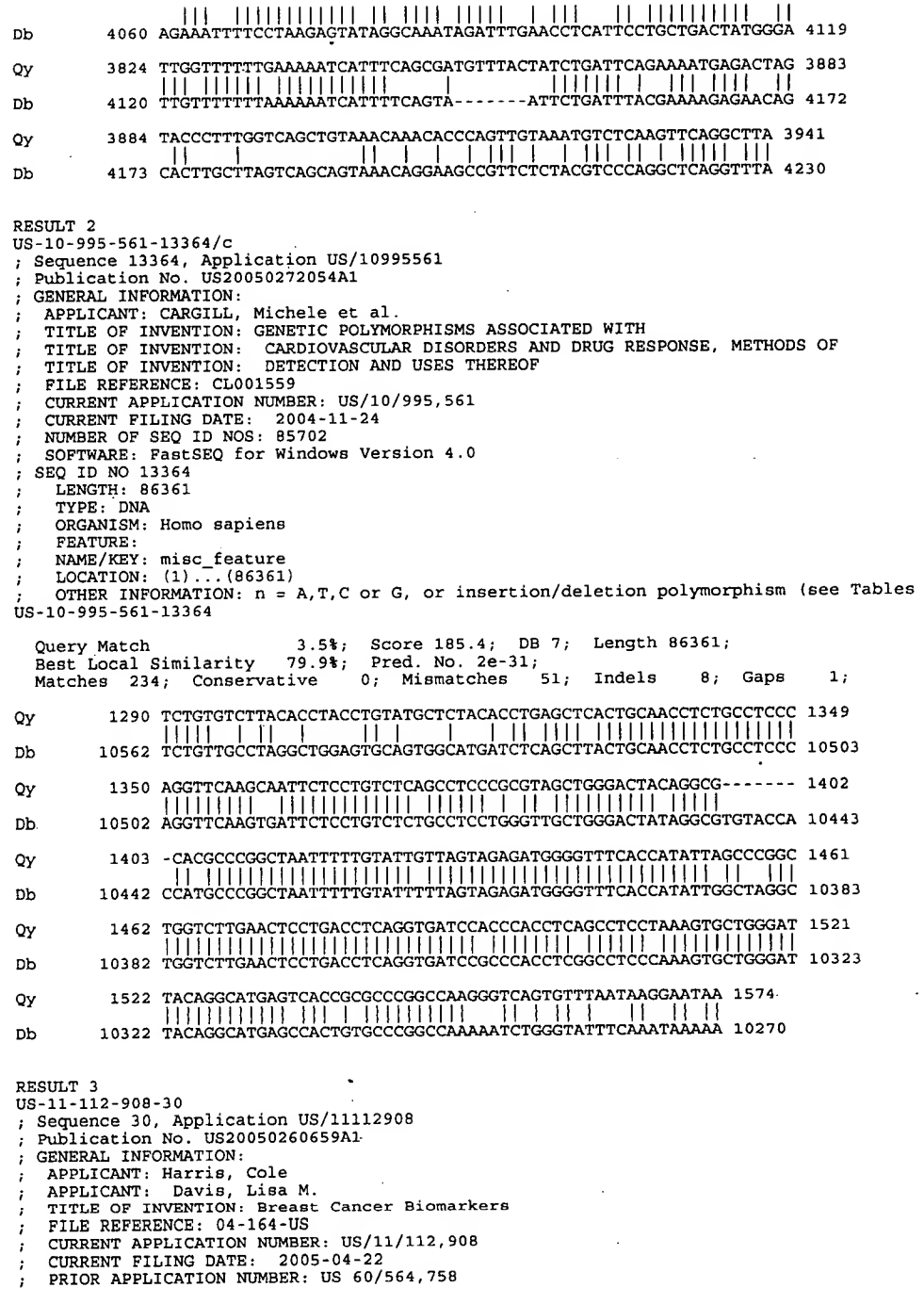
ALIGNMENTS

RESULT 1
US-11-136-527-717
; Sequence 717, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 717
; LENGTH: 16525
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-717

Query Match 3.6%; Score 190.8; DB 8; Length 16525;
Best Local Similarity 55.9%; Pred. No. 6.1e-33;
Matches 871; Conservative 0; Mismatches 542; Indels 145; Gaps 21;

```
Qy       2387 CTTGGCTCCAGGCTCCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGA 2446
             | ||||||| |||||||||||||| ||||||| |||| |||||| | ||  || ||||
Db       2815 CCTGGCTCCTGGCTCCAGAAAGGATATGGAGATGGAATATAGTCTCCCTGAACATTTGGA 2874

Qy       2447 GGGGACAGTGTTTCCTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTG 2506
               || |||||||||||||| |||||| | | |||   ||||   |||| |||||||||||
Db       2875 ATGGCCAGTGTTTCCTCAGTGGGAAAAGAGTCTCTGTGTCC---AGAAATCCAGGAGGTG 2931

Qy       2507 GGGACTGCAGGGAGTGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAA 2566
             ||||||||||||||| | | |           || |    ||  | ||||||||||||||
Db       2932 GGGACTGCAGGGAGGGCTGCTG----------GCCTGCCAGGAGTGACAGGAAGGTGAAA 2981

Qy       2567 AGGGCAAGGCTGAAGCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGT 2626
             ||||  ||||| || ||  |||||||||   | || |   || | |||||  | | ||
Db       2982 AGGG-TAGGCTAAATCTCACCAGATGTTCGTCGCTGCTGGTGGAGTAGGGAGGCTCCTGT 3040

Qy       2627 TGCTTCCTGTGAGCCTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGA 2686
             | || ||   | |||       | |||||  |||| ||||||||    ||||| | ||||
Db       3041 TTCTCCCACAGGGCC-------CATTTCTGGGCTTAGAGGAGAACGGTTCTATCTTATGA 3093
```





RESULT 2
US-10-995-561-13364/c
; Sequence 13364, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13364
; LENGTH: 86361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(86361)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-10-995-561-13364

Query Match 3.5%; Score 185.4; DB 7; Length 86361;
Best Local Similarity 79.9%; Pred. No. 2e-31;
Matches 234; Conservative 0; Mismatches 51; Indels 8; Gaps 1;

RESULT 3
US-11-112-908-30
; Sequence 30, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758

```
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
;   LENGTH: 143389
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-30

  Query Match             3.5%;  Score 185.2;  DB 8;  Length 143389;
  Best Local Similarity   79.4%;  Pred. No. 2.7e-31;
  Matches  235;  Conservative    0;  Mismatches   53;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || |||  | |||||  |  | |      || |    |   | || ||||||| ||||||
Db     113274 AGAGTGTTGCTCTGTCACCCAGATTGGAGTGCAGTGGCACAATCTCAGCTCACCGCAACC 113333

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || |||||||||||||||||||||||||| |||||||||||| |||| ||||||||||
Db     113334 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGGTGGGACTACAG 113393

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
              |||        |||||| |||||||||||||||| ||||||||||||||||||||||||
Db     113394 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 113453

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
             || | | |||||||||||||||||||||||||||  |||||||||||| |||||| |||
Db     113454 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCTCGGCCTCCCAAA 113513

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
             |||||||||||||||  |||| ||||| ||||||||     | | | ||| || | |
Db     113514 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTTTTGACTCTTTTATGA 113569


RESULT 4
US-11-112-908-24
; Sequence 24, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
;   LENGTH: 150314
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-24

  Query Match             3.5%;  Score 185.2;  DB 8;  Length 150314;
  Best Local Similarity   79.4%;  Pred. No. 2.8e-31;
  Matches  235;  Conservative    0;  Mismatches   53;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || |||  | |||||  |  | |      || |    |   | || ||||||| ||||||

Db     27741 AGAGTGTTGCTCTGTCACCCAGATTGGAGTGCAGTGGCACAATCTCAGCTCACCGCAACC 27800

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || |||||||||||||||||||||||||| |||||||||||| |||| ||||||||||
Db     27801 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGGTGGGACTACAG 27860

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
              |||        |||||| |||||||||||||||| ||||||||||||||||||||||||
Db     27861 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 27920

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
             || | | |||||||||||||||||||||||||||  |||||||||||| |||||| |||
Db     27921 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCTCGGCCTCCCAAA 27980

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
             |||||||||||||||  |||| ||||| ||||||||     | | | ||| || | |
Db     27981 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTTTTGACTCTTTTATGA 28036


RESULT 5
US-11-112-908-28
; Sequence 28, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 166020
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-28

  Query Match             3.5%;  Score 185.2;  DB 8;  Length 166020;
  Best Local Similarity   79.4%;  Pred. No. 2.9e-31;
  Matches  235;  Conservative    0;  Mismatches   53;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || |||  | |||||  |  | |      || |    |   | || ||||||| ||||||
Db     159755 AGAGTGTTGCTCTGTCACCCAGATTGGAGTGCAGTGGCACAATCTCAGCTCACCGCAACC 159814

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || |||||||||||||||||||||||||| |||||||||||| |||| ||||||||||
Db     159815 TCCGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCGAGTAGGTGGGACTACAG 159874

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
              |||        |||||| |||||||||||||||| ||||||||||||||||||||||||
Db     159875 GCGCCCGCCACCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATA 159934

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
             || | | |||||||||||||||||||||||||||  |||||||||||| |||||| |||
Db     159935 TTGGTCAGGCTGGTCTTGAACTCCTGACCTCAGGCAATCCACCCACCTCGGCCTCCCAAA 159994

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAA 1567
             |||||||||||||||  |||| ||||| ||||||||     | | | ||| || | |
Db     159995 GTGCTGGGATTACAGGTGTGAGCCACCGTGCCCGGCCTGTTTTGACTCTTTTATGA 160050


RESULT 6
US-10-995-561-13440/c
```

```
; Sequence 13440, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13440
;   LENGTH: 60754
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13440

  Query Match             3.5%;  Score 184; DB 7;  Length 60754;
  Best Local Similarity   71.9%;  Pred. No. 3.6e-31;
  Matches  256;  Conservative    1;  Mismatches   91;  Indels    8;  Gaps    1;

Qy       1283 GTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCT 1342
             ||   | |||||  |  |  |   | || |         | || |||||||||||||||:
Db       9703 GTCTCGCTCTGTCGCCCAGGCTGGCATGCAGTGGTACGATCTCAGCTCACTGCAACCTCY 9644

Qy       1343 GCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG 1402
             | ||||| |||||||||| ||| | ||| |||||||||| | ||||||||||||||||| |
Db       9643 GTCTCCCGGGTTCAAGCGATTTTTCTGCCTCAGCCTCCAGAGTAGCTGGGACTACAGGAG 9584

Qy       1403 C--------ACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTA 1454
             |        | ||| |||||||||| |||| |||||||||||||||||||||||||  ||
Db       9583 CCTGTCACTATGCCTGGCTAATTTTTATATTTTTAGTAGAGATGGGGTTTCACCAAGTTG 9524

Qy       1455 GCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTG 1514
             ||| |||||||||||||||||||||||| |||||||||| |||| |||||| ||||||
Db       9523 GCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCCACCCTCCTCGGCCTCCCAAAGTG 9464

Qy       1515 CTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAA 1574
             |||||||||||||||| || ||| ||||||||||||    |     | | |  |  |||
Db       9463 CTGGGATTACAGGCATTAGCCACTGCGCCCGGCCAACAATTCAAATCTTAACAAACAAAA 9404

Qy       1575 CTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGATAATTTCAGG 1630
                ||| |  | |||| || |  ||||| | || | | |   ||| | ||
Db       9403 TAATAATAATAAAATAAAGAAAGAAAAAAACACAAAATATCAGAGCATATTACGGG 9348


RESULT 7
US-10-995-561-13274
; Sequence 13274, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13274
;   LENGTH: 415117
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(415117)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13274

  Query Match             3.5%;  Score 183.4;  DB 7;  Length 415117;
  Best Local Similarity   76.5%;  Pred. No. 1.1e-30;
  Matches  241;  Conservative    0;  Mismatches   66;  Indels    8;  Gaps    1;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || ||   | ||||  |  || |     || |    |   | || ||||||||||||||
Db      60473 AGAGTCTTGCTCTGTCACCCACGCTGTAGTGCAATGGCGCAATCTCAGCTCACTGCAACC 60532

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             || |||||||||||||||  |||||||| |||||||||| | |||||||||| |||||
Db      60533 TCCGCCTCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAG 60592

Qy       1400 GCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATA 1451
             |||        || |||||||||||||||||| |||||||||||||||||| |||||
Db      60593 GTGAGTGCCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTACCATG 60652

Qy       1452 TTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAA 1511
             || ||| |||||||||| ||||||||||||||||||||||||||||||  ||||||  |||
Db      60653 TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAA 60712

Qy       1512 GTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAA 1571
             |||||||||||||||| | || |||||||| |||| |||   | |  ||  || | |
Db      60713 GTGCTGGGATTACAGGCGTAAGCCACCGCGCCTGGCCTAGGCCAAATAATTTTTATGAAC 60772

Qy       1572 TAACTTGAATGGTTT 1586
             |  || ||   | ||
Db      60773 TGTCTGGAGAAGCTT 60787


RESULT 8
US-10-995-561-13379
; Sequence 13379, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13379
;   LENGTH: 14804
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13379

  Query Match             3.4%;  Score 179.6;  DB 7;  Length 14804;
  Best Local Similarity   80.0%;  Pred. No. 1.9e-30;
  Matches  224;  Conservative    2;  Mismatches   46;  Indels    8;  Gaps    1;

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
             | || |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      13508 ATCTCAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCC 13567

Qy       1381 CGCGTAGCTGGGACTACAGGC--------GCACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
             |  ||||||||| |||||||           ||||||| ||||||||||||||| ||||||
Db      13568 CAAGTAGCTGGGATTACAGGCACGCACCACCACGCCCAGCTAATTTTTGTATTCTTAGTA 13627

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
             |||| |||||||||||||| || ||| ||||||||| |||||||||||||||  |||||||
Db      13628 GAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAATGATCCA 13687

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
             |||||||| | |||| |||||||||||||||||||||||| |||||||||:|||| |
Db      13688 CCCACCTCGGTCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCYGGCCCCGT 13747

Qy       1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAA 1592
                 :||||     ||  ||    ||||  ||   ||
Db      13748 TATTTCAKTTAAGCCTCAAATACAAATATGGAGTAAGCAA 13787


RESULT 9
```

```
US-10-995-561-13331/c
; Sequence 13331, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;  TITLE OF INVENTION:  DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001559
;  CURRENT APPLICATION NUMBER: US/10/995,561
;  CURRENT FILING DATE:  2004-11-24
;  NUMBER OF SEQ ID NOS: 85702
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13331
;   LENGTH: 98716
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-995-561-13331

  Query Match             3.4%;  Score 179.6;  DB 7;  Length 98716;
  Best Local Similarity   80.0%;  Pred. No. 4.3e-30;
  Matches  224;  Conservative    2;  Mismatches   46;  Indels    8;  Gaps    1;

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
             | || ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      75944 ATCTCAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCC 75885

Qy       1381 CGCGTAGCTGGGACTACAGGC--------GCACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
             |  |||||||||| |||||||          ||||||| |||||||||||||| ||||||
Db      75884 CAAGTAGCTGGGATTACAGGCACGCACCACCACGCCCAGCTAATTTTTGTATTCTTAGTA 75825

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
             ||||| |||||||||||| || ||| ||||||||| |||||||||||||  |||||||
Db      75824 GAGACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAAATGATCCA 75765

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
             |||||||| | |||| |||||||||||||||||||||||| |||||||||:||||  |
Db      75764 CCCACCTCGGTCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCYGGCCCCGT 75705

Qy       1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAA 1592
                 :||||     ||  ||    ||||  ||   ||
Db      75704 TATTTCAKTTAAGCCTCAAATACAAATATGGAGTAAGCAA 75665


RESULT 10
US-11-121-086-60
; Sequence 60, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
;   LENGTH: 191091
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-60

  Query Match             3.4%;  Score 179.6;  DB 8;  Length 191091;
  Best Local Similarity   79.9%;  Pred. No. 5.6e-30;
  Matches  227;  Conservative    0;  Mismatches   49;  Indels    8;  Gaps    1;

Qy       1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349
             |||||  | ||  |     || |    |   | || ||||||||||||||||  ||||||
Db     104701 TCTGTCCCCTAGGCTGGAGTGCAGTGGCACAATCTTAGCTCACTGCAACCTCCACCTCCC 104760

Qy       1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGC-------- 1401
             |||||| |||||||||||||||||||||||||| ||||||||||||||||||
Db     104761 AGGTTCCAGCAATTCTCCTGTCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACACACTA 104820

Qy       1402 GCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461
             |||||||  |||||||||||||| ||||| ||||  |||||||||||||| | | |||
Db     104821 TCACGCCCATCTAATTTTTGTATTTTTAGTGGAGACAGGGTTTCACCATATTGGTCAGGC 104880

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
             |||||| |||||||||||||||||||||||||||||||| |||| |||||| ||||||||||||
Db     104881 TGGTCTCGAACTCCTGACCTCAGGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGAT 104940

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAAT 1565
             ||||||| |||| ||||| |||||||| | |      | ||||||
Db     104941 TACAGGCGTGAGCCACCGAGCCCGGCCCATGTCAGTTATTTAAT 104984


RESULT 11
US-11-112-908-61/c
; Sequence 61, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
;   LENGTH: 159497
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-61

  Query Match             3.4%;  Score 179;  DB 8;  Length 159497;
  Best Local Similarity   81.0%;  Pred. No. 7.1e-30;
  Matches  221;  Conservative    0;  Mismatches   50;  Indels    2;  Gaps    1;

Qy       1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
             | |||  | |||||    ||  |     || |    |   | || ||||||||||||||||
Db     100954 GAGTGTTGCTCTGTCAACTAGGCTGGAATGCAGTGGCATGATCTCAGCTCACTGCAACCT 100895

Qy       1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
             ||||||||  ||||||||| |||||||||||||||||||||   |||| ||||| ||||||
Db     100894 CTGCCTCCTGGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCAAGTAGTTGGGATTACAGG 100835

Qy       1401 C--GCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCC 1458
             |   || |||||||||||||||||| |||||||||||||||||||||||||||| |||| |
Db     100834 CCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGGCA 100775

Qy       1459 GGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGG 1518
             ||||||||| |||||||||||||| ||||||||| | |||| |||||| |||||  |||
Db     100774 GGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACTCGCCTCGGCCTCCCAAAGTTTTGG 100715

Qy       1519 GATTACAGGCATGAGTCACCGCGCCCGGCCAAG 1551
             ||||||||||||||| ||| ||||| ||||| |
Db     100714 GATTACAGGCATGAGCCACTGCGCCTGGCCATG 100682


RESULT 12
US-11-112-908-60/c
; Sequence 60, Application US/11112908
; Publication No. US20050260659A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
;   LENGTH: 171427
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-60

  Query Match             3.4%;  Score 179;  DB 8;  Length 171427;
  Best Local Similarity   81.0%;  Pred. No. 7.4e-30;
  Matches  221;  Conservative    0;  Mismatches   50;  Indels    2;  Gaps    1;

Qy       1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
             | |||  | |||||   ||  |    || |    |  | || ||||||||||||||||
Db       7090 GAGTGTTGCTCTGTCAACTAGGCTGGAATGCAGTGGCATGATCTCAGCTCACTGCAACCT 7031

Qy       1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
             ||||||||  |||||||||| ||||||||||||||||||||||  |||| ||||| ||||||
Db       7030 CTGCCTCCTGGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCAAGTAGTTGGGATTACAGG 6971

Qy       1401 C--GCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCC 1458
             |   || ||||||||||||||||||| ||||||||||||||||||||||| |||| |
Db       6970 CCACCATGCCCGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTAGGCA 6911

Qy       1459 GGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGG 1518
             ||||||||| |||||||||||||| ||||||||| | |||| |||||| |||||  |||
Db       6910 GGCTGGTCTCGAACTCCTGACCTCAAGTGATCCACTCGCCTCGGCCTCCCAAAGTTTTGG 6851

Qy       1519 GATTACAGGCATGAGTCACCGCGCCCGGCCAAG 1551
             ||||||||||||||| ||| ||||| ||||| |
Db       6850 GATTACAGGCATGAGCCACTGCGCCTGGCCATG 6818


RESULT 13
US-10-775-169-82/c
; Sequence 82, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Burczynski, Michael
;  APPLICANT:  Twine, Natalie
;  APPLICANT:  Dorner, Andrew
;  APPLICANT:  Trepicchio, William
;  TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
;  FILE REFERENCE: AM101080 (031896-013000)
;  CURRENT APPLICATION NUMBER: US/10/775,169
;  CURRENT FILING DATE:  2004-02-11
;  NUMBER OF SEQ ID NOS: 5278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
;   LENGTH: 127917
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-775-169-82

  Query Match             3.4%;  Score 178.4;  DB 7;  Length 127917;
  Best Local Similarity   77.2%;  Pred. No. 8.9e-30;
  Matches  233;  Conservative    0;  Mismatches   61;  Indels    8;  Gaps    1;

Qy       1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
             | ||   | |||||  |  |  |    || |    |  | ||  |||||||||||| ||
Db      99645 GAGTCTTGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCATGATCTCGGCTCACTGCAAACT 99586

Qy       1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
              |  ||||||| |||||||| |||||||| |||||||||||| |||||||||| ||||||
Db      99585 CCACCTCCCAAGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGG 99526

Qy       1401 CG--------CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATAT 1452
              |        ||| ||| |||||||||||||| |||||||||||||||||||||||||||
Db      99525 TGCCCACCACCACACCCAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATAT 99466

Qy       1453 TAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAG 1512
              | ||| | ||||||| |||||||||||||||||||||||||| |||||||||| | ||
Db      99465 TGGCCAGACTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCCAGAG 99406

Qy       1513 TGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAAT 1572
              |||||||||| |||| |||| |||||||||||||  ||| |||   || | | | |
Db      99405 TGCTGGGATTATAGGCGTGAGCCACCGCGCCCGGCCTTGGGACAGGTCTTTAAAGGAAGG 99346

Qy       1573 AA 1574
              ||
Db      99345 AA 99344


RESULT 14
US-11-112-908-57
; Sequence 57, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;  APPLICANT: Harris, Cole
;  APPLICANT:  Davis, Lisa M.
;  TITLE OF INVENTION: Breast Cancer Biomarkers
;  FILE REFERENCE: 04-164-US
;  CURRENT APPLICATION NUMBER: US/11/112,908
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: US 60/564,758
;  PRIOR FILING DATE: 2004-04-23
;  PRIOR APPLICATION NUMBER: US 60/575,978
;  PRIOR FILING DATE: 2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/631,702
;  PRIOR FILING DATE: 2004-11-30
;  PRIOR APPLICATION NUMBER: US 60/633,826
;  PRIOR FILING DATE: 2004-12-07
;  NUMBER OF SEQ ID NOS: 511
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
;   LENGTH: 161994
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-57

  Query Match             3.4%;  Score 177.8;  DB 8;  Length 161994;
  Best Local Similarity   86.0%;  Pred. No. 1.3e-29;
  Matches  197;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy       1325 GAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCG 1384
             |||  || ||| | |||  |||||  ||||||||| ||||||||| ||||||||||||
Db     131831 GAGTGCAATGCGAGCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG 131890

Qy       1385 TAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTT 1444
             ||||||||| |||||| ||| |||| |||||||||| |||| ||||||||||||||||||
Db     131891 TAGCTGGGATTACAGGGGCAGGCCCAGCTAATTTTTATATTTTTAGTAGAGATGGGGTTT 131950

Qy       1445 CACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCC 1504
             |||||| || ||| |||||||||||||||||||| |||||   ||  ||| |||  |||
Db     131951 CACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACTTCAGGCAGTCTGCCCGCCTGGGCC 132010

Qy       1505 TCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGG 1553
             ||| |||||||||||||||||||||| ||||||||||||||||||||
Db     132011 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCAAGGG 132059
```

RESULT 15
US-11-112-908-59
; Sequence 59, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 168656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-59

Query Match 3.4%; Score 177.8; DB 8; Length 168656;
Best Local Similarity 86.0%; Pred. No. 1.4e-29;
Matches 197; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```
Qy       1325 GAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCG 1384
             ||| || ||| | |||  |||||  ||||||||| ||||||||| |||||||||||| |
Db       1285 GAGTGCAATGCGAGCTCCACCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAG 1344

Qy       1385 TAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTT 1444
             ||||||||| |||||| ||| |||| |||||||||| |||| ||||||||||||||||||
Db       1345 TAGCTGGGATTACAGGGGCAGGCCCAGCTAATTTTTATATTTTAGTAGAGATGGGGTTT 1404

Qy       1445 CACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCC 1504
             |||||| || ||| |||||||||||||||||||| |||||   ||  ||| |||  |||
Db       1405 CACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACTTCAGGCAGTCTGCCCGCCTGGGCC 1464

Qy       1505 TCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGG 1553
             ||| |||||||||||||||||||||| ||||||||||||||||||
Db       1465 TCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCAAGGG 1513
```

Search completed: January 26, 2006, 10:16:38
Job time : 525 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 26, 2006, 02:50:21 ; Search time 17273 Seconds
(without alignments)
16872.686 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagtttacctc.....tcgggcatgagccagcaagg 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUSB_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US076_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US079_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US099E_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US100B_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US101_COMB.seq:*
43: /cgn2_6/ptodata/1/pna/US102A_COMB.seq:*
44: /cgn2_6/ptodata/1/pna/US102B_COMB.seq:*
45: /cgn2_6/ptodata/1/pna/US103A_COMB.seq:*
46: /cgn2_6/ptodata/1/pna/US103B_COMB.seq:*
47: /cgn2_6/ptodata/1/pna/US103C_COMB.seq:*
48: /cgn2_6/ptodata/1/pna/US103D_COMB.seq:*
49: /cgn2_6/ptodata/1/pna/US103E_COMB.seq:*
50: /cgn2_6/ptodata/1/pna/US103F_COMB.seq:*
51: /cgn2_6/ptodata/1/pna/US104_COMB.seq:*
52: /cgn2_6/ptodata/1/pna/US105_COMB.seq:*
53: /cgn2_6/ptodata/1/pna/US106A_COMB.seq:*
54: /cgn2_6/ptodata/1/pna/US106B_COMB.seq:*
55: /cgn2_6/ptodata/1/pna/US107A_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US107B_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US107C_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US107D_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US107E_COMB.seq:*
60: /cgn2_6/ptodata/1/pna/US107F_COMB.seq:*
61: /cgn2_6/ptodata/1/pna/US107G_COMB.seq:*
62: /cgn2_6/ptodata/1/pna/US108_COMB.seq:*
63: /cgn2_6/ptodata/1/pna/US109A_COMB.seq:*
64: /cgn2_6/ptodata/1/pna/US109B_COMB.seq:*
65: /cgn2_6/ptodata/1/pna/US109C_COMB.seq:*
66: /cgn2_6/ptodata/1/pna/US110A_COMB.seq:*
67: /cgn2_6/ptodata/1/pna/US110B_COMB.seq:*
68: /cgn2_6/ptodata/1/pna/US110C_COMB.seq:*
69: /cgn2_6/ptodata/1/pna/US110D_COMB.seq:*
70: /cgn2_6/ptodata/1/pna/US111A_COMB.seq:*
71: /cgn2_6/ptodata/1/pna/US111B_COMB.seq:*
72: /cgn2_6/ptodata/1/pna/US112_COMB.seq:*
73: /cgn2_6/ptodata/1/pna/US117_COMB.seq:*
74: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
75: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
76: /cgn2_6/ptodata/1/pna/US602A_COMB.seq:*
77: /cgn2_6/ptodata/1/pna/US602B_COMB.seq:*
78: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*
79: /cgn2_6/ptodata/1/pna/US604A_COMB.seq:*
80: /cgn2_6/ptodata/1/pna/US604B_COMB.seq:*
81: /cgn2_6/ptodata/1/pna/US605_COMB.seq:*
82: /cgn2_6/ptodata/1/pna/US606_COMB.seq:*
83: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5271	100.0	5271	22	US-09-227-881-34	Sequence 34, Appl
2	5271	100.0	5271	43	US-10-244-633-34	Sequence 34, Appl
3	5271	100.0	6169	19	US-08-938-669-3	Sequence 3, Appli
4	5271	100.0	6169	22	US-09-227-881-3	Sequence 3, Appli
5	5271	100.0	6169	43	US-10-244-633-3	Sequence 3, Appli
6	5246.4	99.5	5300	19	US-08-938-669-1	Sequence 1, Appli
7	5246.4	99.5	5300	22	US-09-227-881-1	Sequence 1, Appli
8	5246.4	99.5	5300	38	US-09-985-637A-1	Sequence 1, Appli
9	5246.4	99.5	5300	43	US-10-244-633-1	Sequence 1, Appli
10	5246.4	99.5	5300	61	US-10-741-339-1	Sequence 1, Appli
11	5232.4	99.3	37252	40	US-10-087-192-1228	Sequence 1228, Ap
12	5224.4	99.1	5304	19	US-08-938-669-2	Sequence 2, Appli
13	5224.4	99.1	5304	22	US-09-227-881-2	Sequence 2, Appli
14	5224.4	99.1	5304	43	US-10-244-633-2	Sequence 2, Appli
15	4925.4	93.4	7369	75	US-60-172-360-23886	Sequence 23886, A
16	4017.4	76.2	6000	52	US-10-509-595-1	Sequence 1, Appli
17	1804.4	34.2	2800	23	US-09-366-952-1	Sequence 1, Appli
18	1804.4	34.2	2800	43	US-10-278-698-294	Sequence 294, App
19	1804.4	34.2	2800	43	US-10-278-698-808	Sequence 808, App
20	1804.4	34.2	2800	62	US-10-803-557-10	Sequence 10, Appl
21	1804.4	34.2	2800	64	US-10-956-243-1	Sequence 1, Appli
22	1691.6	32.1	2666	17	US-08-791-154-3	Sequence 3, Appli
23	1690	32.1	2397	17	US-08-791-154-1	Sequence 1, Appli

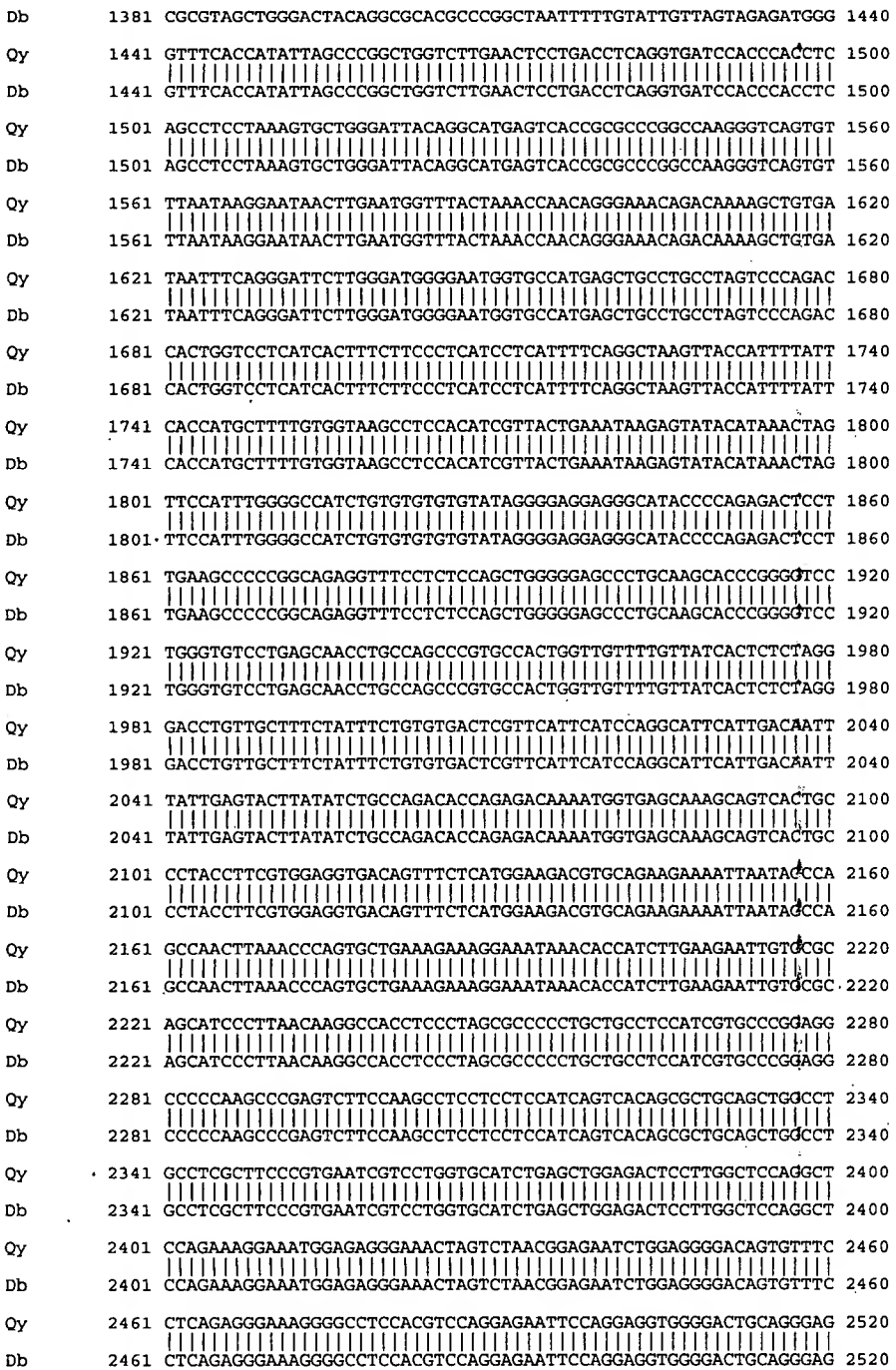
24	1669.6	31.7	1950	17	US-08-791-154-2	Sequence 2, Appli
25	631.6	12.0	632	36	US-09-925-065A-905501	Sequence 905501,
c 26	629.6	11.9	630	36	US-09-925-065A-917000	Sequence 917000,
27	548	10.4	573	45	US-10-301-480-418443	Sequence 418443,
28	548	10.4	573	45	US-10-301-480-1031852	Sequence 1031852,
29	548	10.4	573	46	US-10-301-480A-794512	Sequence 794512,
30	548	10.4	573	47	US-10-301-480B-794512	Sequence 794512,
31	548	10.4	573	48	US-10-301-480C-794512	Sequence 794512,
32	546	10.4	571	36	US-09-925-065A-346049	Sequence 346049,
33	432.6	8.2	2313	82	US-60-680-473-5473	Sequence 5473, Ap
34	432.6	8.2	2313	82	US-60-680-544-5473	Sequence 5473, Ap
35	394.6	7.5	545	36	US-09-925-065A-346051	Sequence 346051,
36	394.6	7.5	546	45	US-10-301-480-418445	Sequence 418445,
37	394.6	7.5	546	45	US-10-301-480-1031854	Sequence 1031854,
38	394.6	7.5	546	46	US-10-301-480A-794514	Sequence 794514,
39	394.6	7.5	546	47	US-10-301-480B-794514	Sequence 794514,
40	394.6	7.5	546	48	US-10-301-480C-794514	Sequence 794514,
41	394.4	7.5	1086	2	PCT-US03-38193-927	Sequence 927, App
42	394.4	7.5	1086	43	US-10-240-425-1586	Sequence 1586, Ap
43	394.4	7.5	1086	61	US-10-723-860-927	Sequence 927, App
44	394.4	7.5	1086	61	US-10-756-149-932	Sequence 932, App
45	393	7.5	545	36	US-09-925-065A-346050	Sequence 346050,

ALIGNMENTS

RESULT 1
US-09-227-881-34
; Sequence 34, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-881-34

Query Match 100.0%; Score 5271; DB 22; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

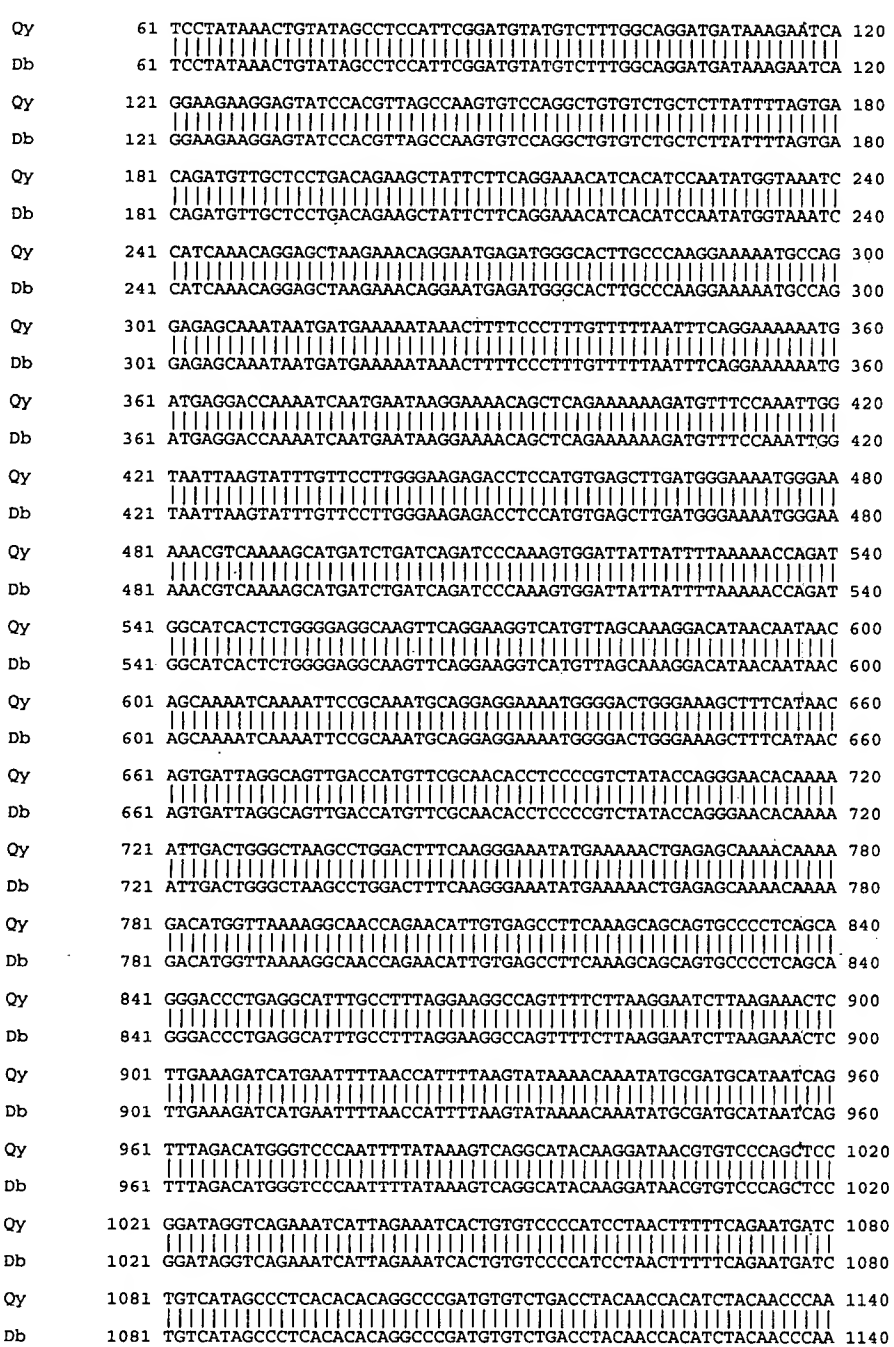

Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATACCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATACCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

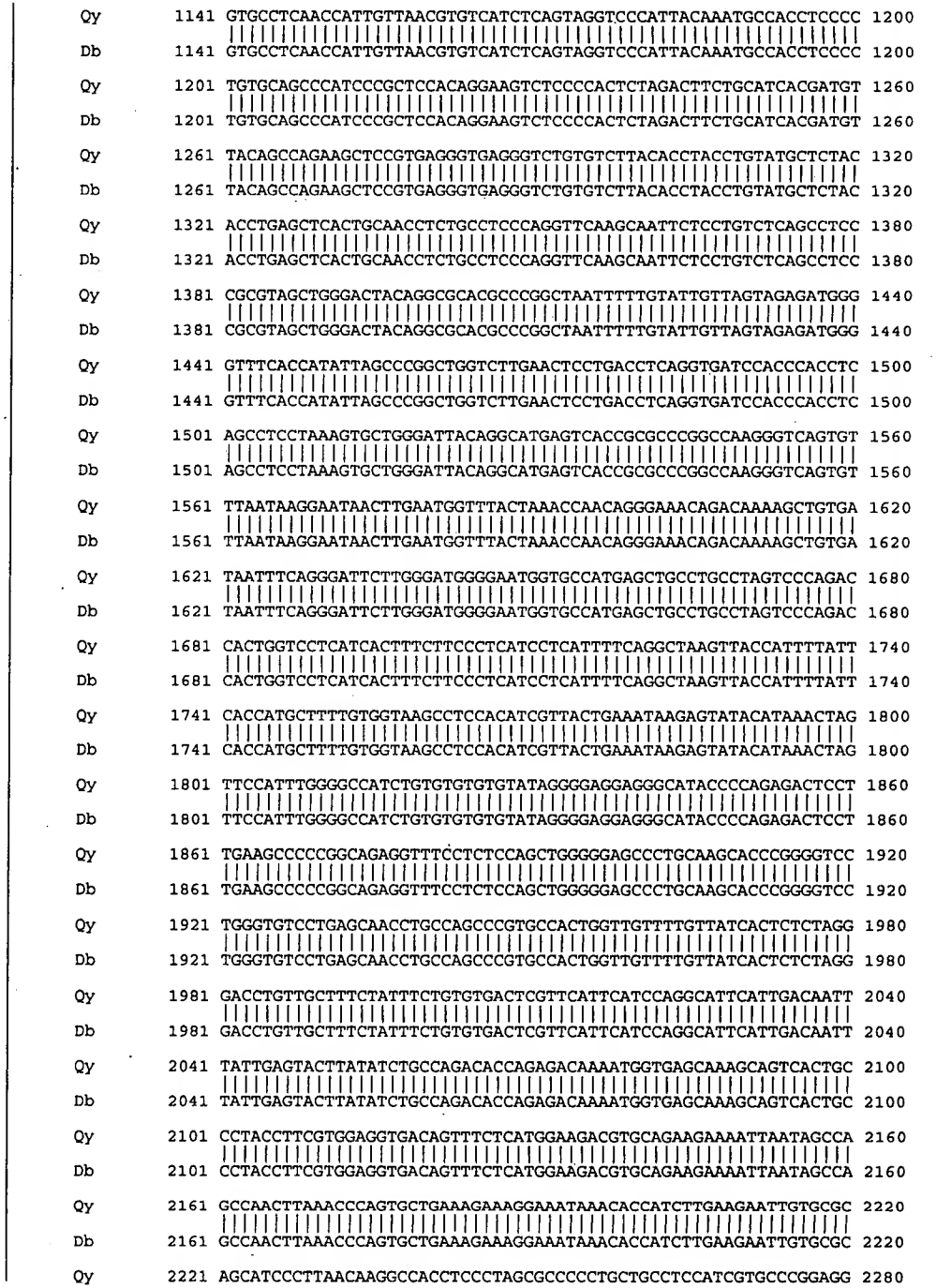
```
Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Qy       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Qy       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Qy       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

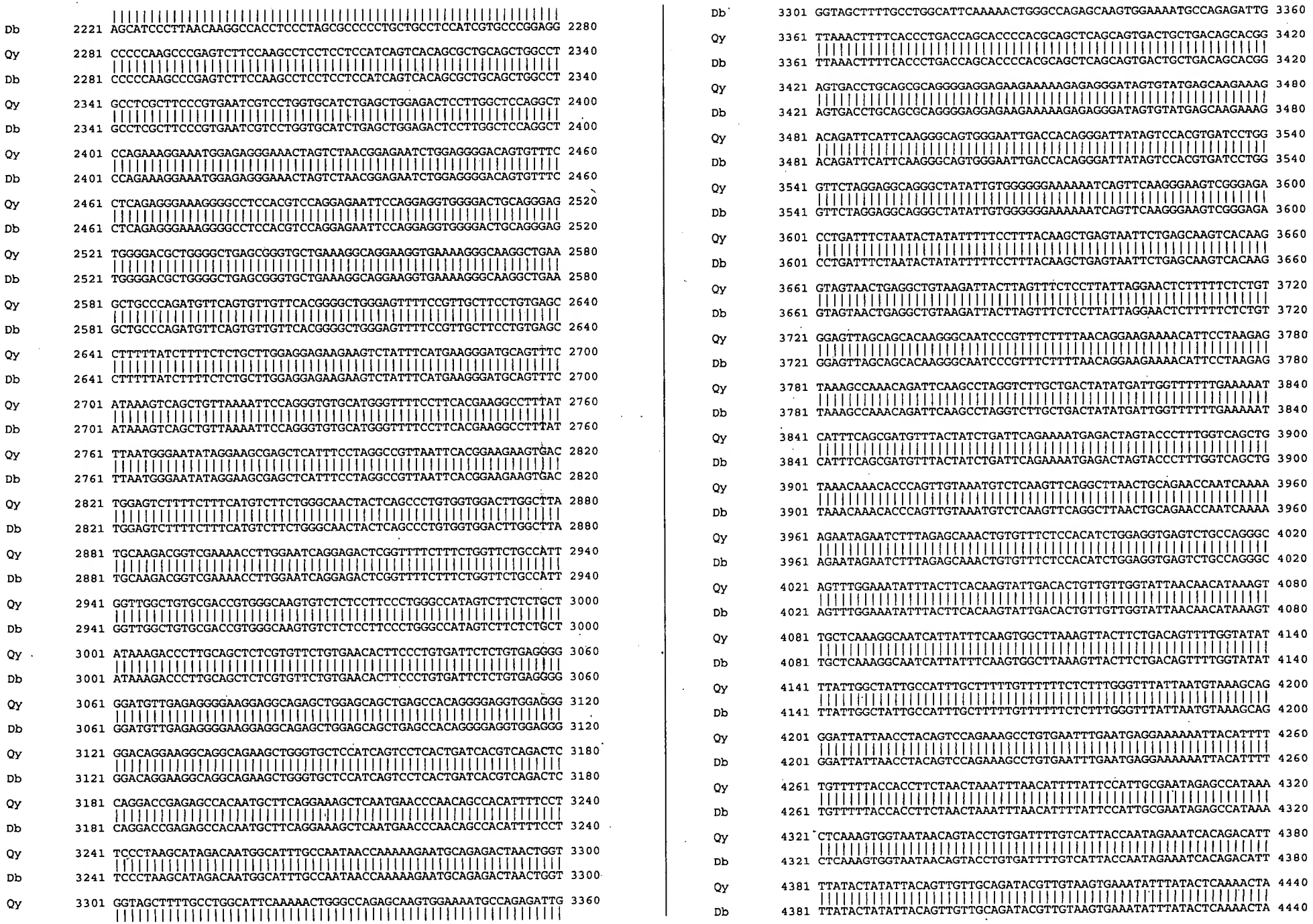
RESULT 2
US-10-244-633-34
; Sequence 34, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 34
; LENGTH: 5271
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-34

Query Match 100.0%; Score 5271; DB 43; Length 5271;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
```


Qy 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Qy 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Db 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Qy 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Qy 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Qy 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140


Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

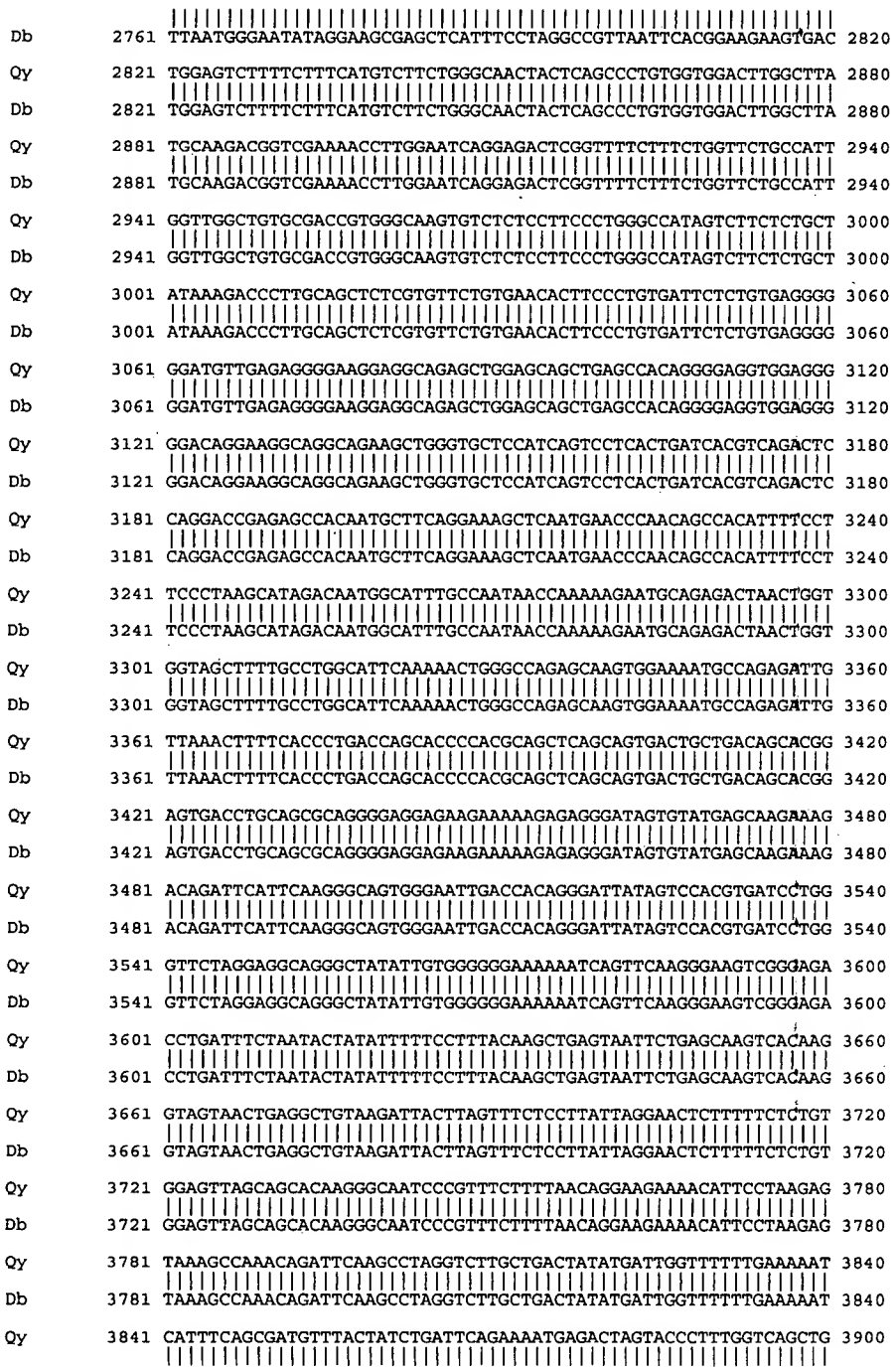

Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

```
Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

```
RESULT 3
US-08-938-669-3
; Sequence 3, Application US/08938669
;  GENERAL INFORMATION:
;    APPLICANT:  Nguyen, Thai D.
;    APPLICANT:  Polansky, Jon R.
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
;    TITLE OF INVENTION:  S
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howrey & Simon
;      STREET:  1299 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004-2402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/938,669
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/791,154
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sira, Serge
;      REGISTRATION NUMBER:  39,445
;      REFERENCE/DOCKET NUMBER:  07425-0034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 383-6857
;      TELEFAX:  202 383-6610
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6169 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-938-669-3

  Query Match             100.0%;  Score 5271;  DB 19;  Length 6169;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
```

```
Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
```


Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Qy 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500
Qy 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Db 4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
Qy 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Db 4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
Qy 4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Db 4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
Qy 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Db 4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
Qy 4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Db 4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
Qy 4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Db 4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
Qy 4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Db 4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
Qy 4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
Db 4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

```
Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271


RESULT 4
US-09-227-881-3
; Sequence 3, Application US/09227881
; GENERAL INFORMATION:
;  APPLICANT: Nguyen, Thai D.
;  APPLICANT: Polansky, Jon R.
;  APPLICANT: Chen, Pu
;  APPLICANT: Chen, Hua
;  TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
;  CURRENT APPLICATION NUMBER: US/09/227,881
;  CURRENT FILING DATE: 1999-01-11
;  EARLIER APPLICATION NUMBER: US 08/938,669
;  EARLIER FILING DATE: 1997-09-26
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
;   LENGTH: 6169
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-227-881-3

  Query Match             100.0%;  Score 5271;  DB 22;  Length 6169;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 5271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
```

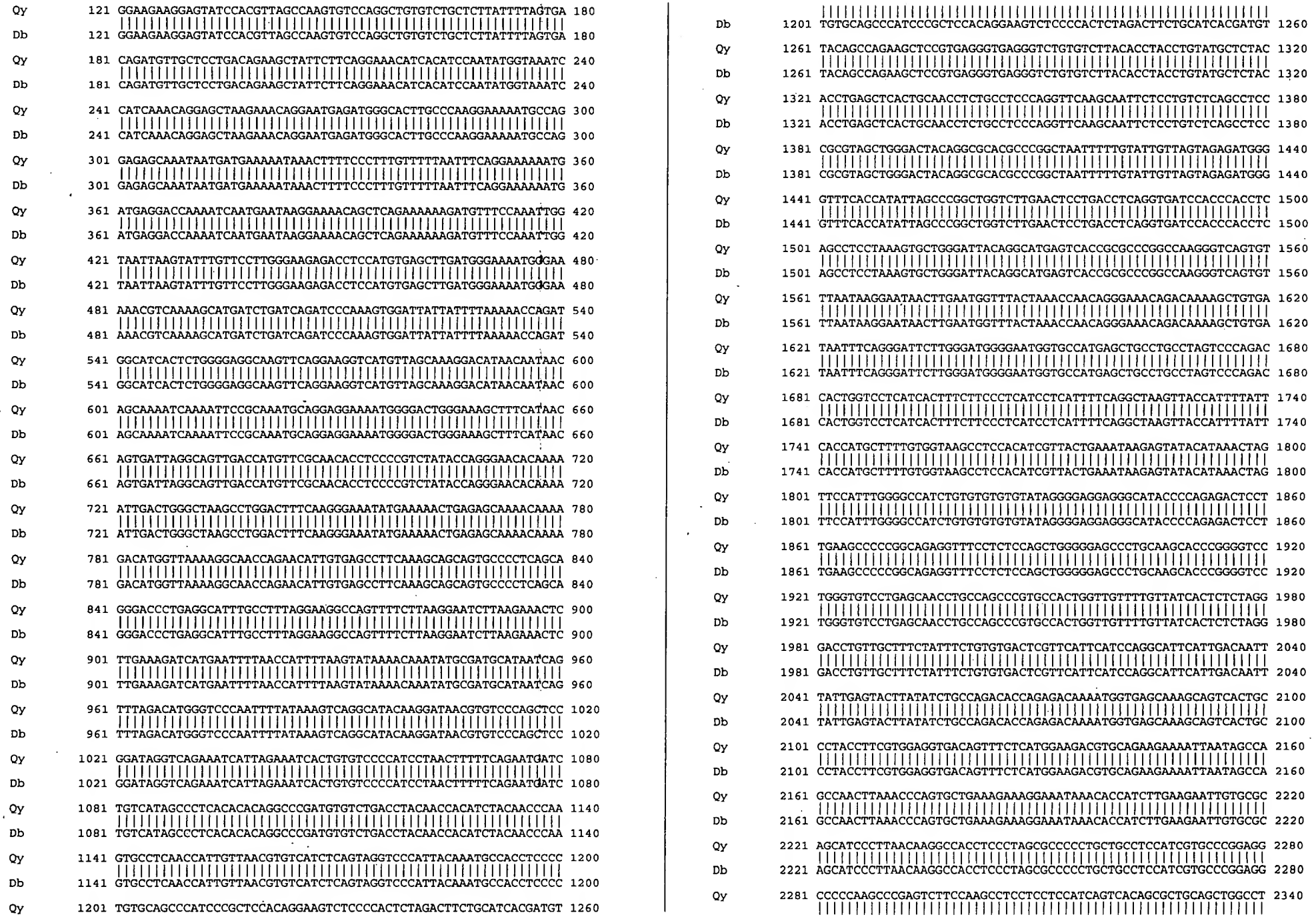
```
Qy      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
```

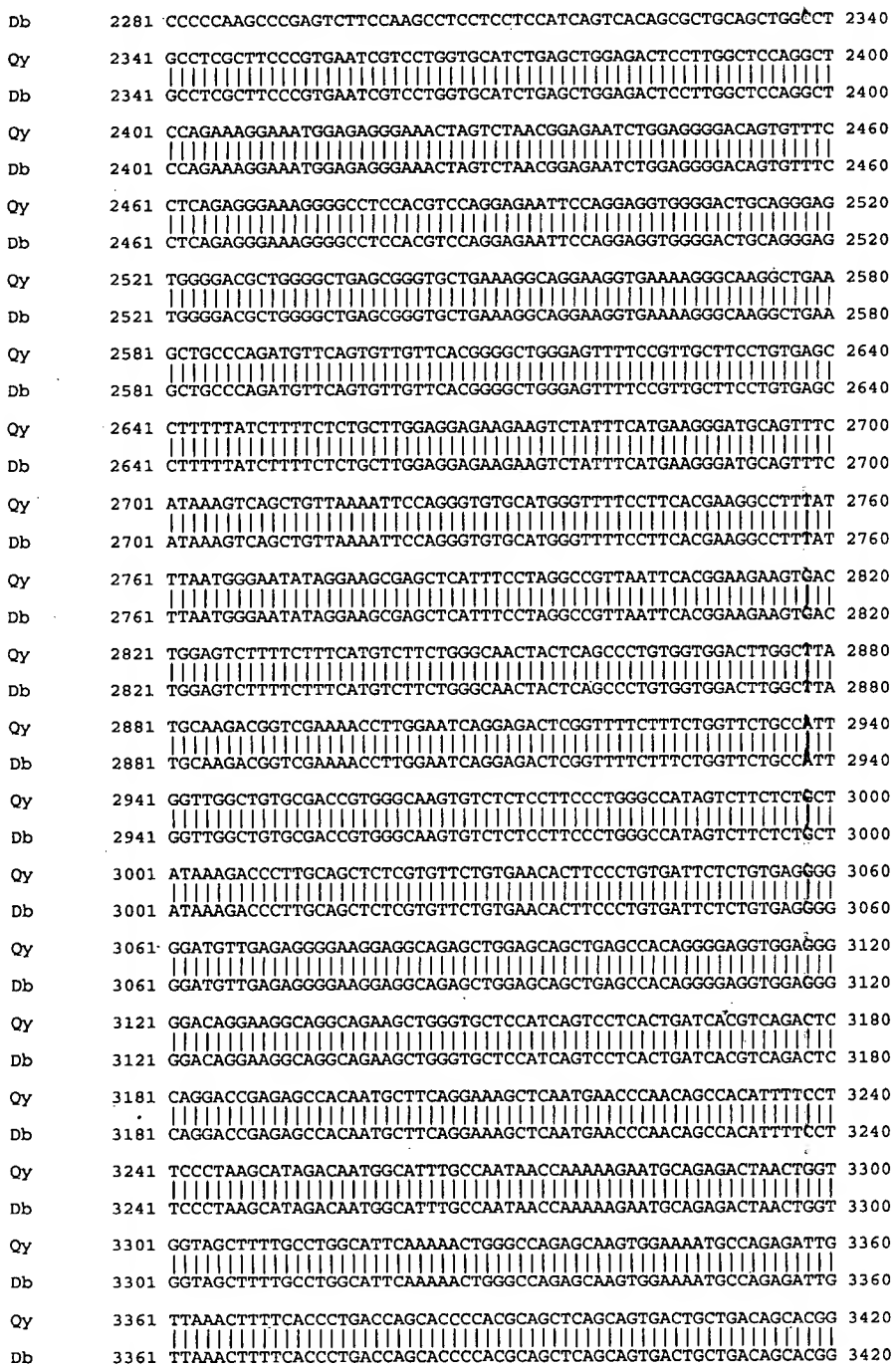
```
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Db       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Db       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Db       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Db       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Qy       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Db       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200

Qy       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Db       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Qy       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Db       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Db       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Db       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271

Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 5
US-10-244-633-3
; Sequence 3, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 3
; LENGTH: 6169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-3

Query Match 100.0%; Score 5271; DB 43; Length 6169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

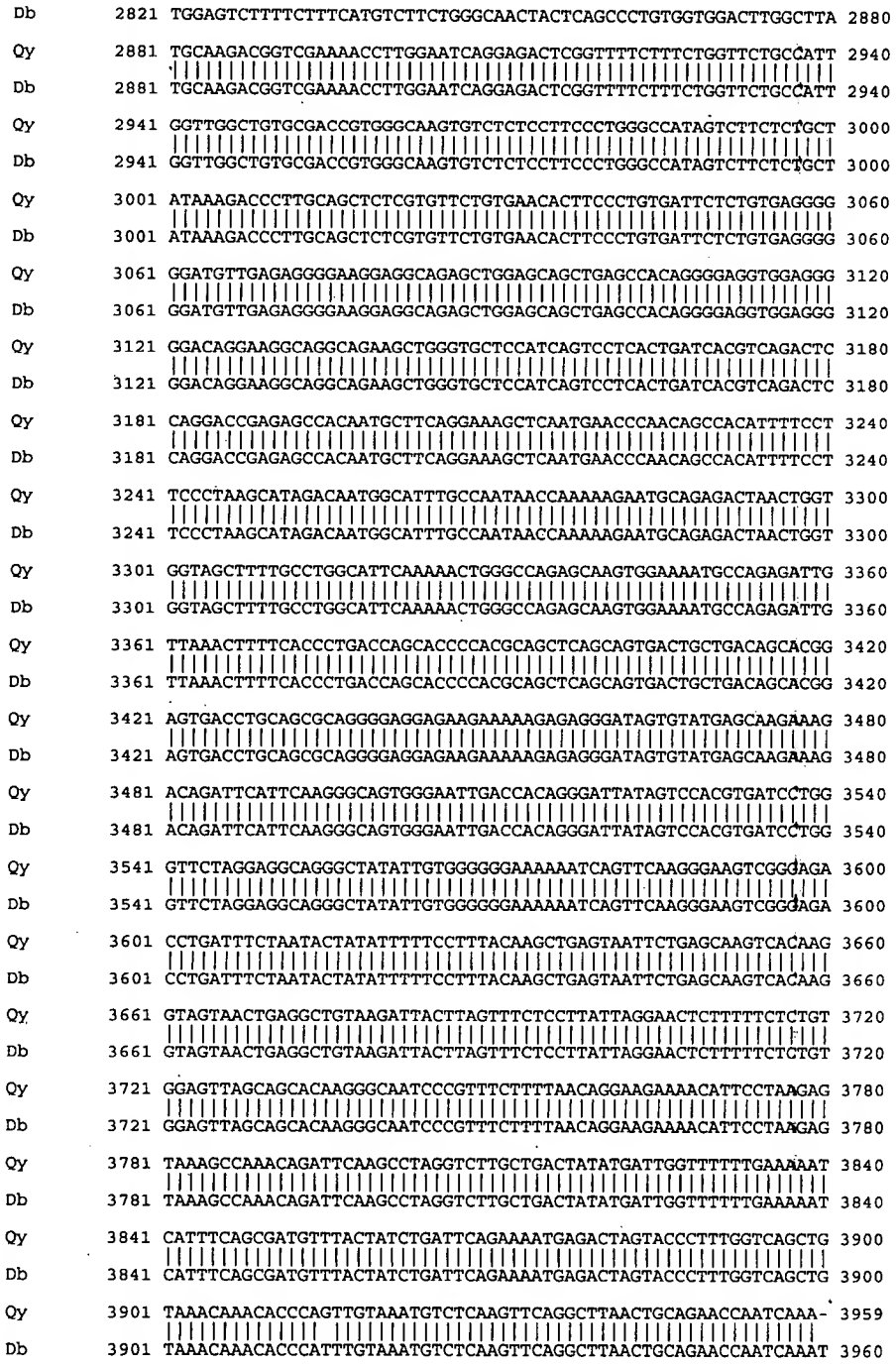
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
```




Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Db 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
Qy 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Db 3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
Qy 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Db 4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
Qy 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Db 4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
Qy 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Db 4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
Qy 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Db 4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
Qy 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Db 4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
Qy 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Db 4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
Qy 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Db 4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
Qy 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500
Db 4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTTAACATATTAATAAAACATGTTTAAA 4500

```
Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271


RESULT 6
US-08-938-669-1
; Sequence 1, Application US/08938669
;  GENERAL INFORMATION:
;    APPLICANT:  Nguyen, Thai D.
;    APPLICANT:  Polansky, Jon R.
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
;    TITLE OF INVENTION:  S
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howrey & Simon
;      STREET:  1299 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004-2402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/938,669
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/791,154
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sira, Serge
;      REGISTRATION NUMBER:  39,445
;      REFERENCE/DOCKET NUMBER:  07425-0034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 383-6857
;      TELEFAX:  202 383-6610
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5300 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-938-669-1

  Query Match             99.5%;  Score 5246.4;  DB 19;  Length 5300;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 5269;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
```

```
Qy    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy    901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy   1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy   1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy   1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy   1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy   1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy   1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy   1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy   2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy   2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy   2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy   2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy   2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy   2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy   2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy   2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy   2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy   2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```


Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy 4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db 4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Db 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

```
Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 7
US-09-227-881-1
; Sequence 1, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-881-1

Query Match 99.5%; Score 5246.4; DB 22; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
```

```
Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
```

```
Db       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
```

```
Db      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy      3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db      3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy      3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db      3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy      4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db      4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy      4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db      4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy      4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db      4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy      4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db      4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Qy      4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db      4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy      4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db      4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy      4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db      4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy      4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db      4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy      4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db      4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy      4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db      4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy      4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db      4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy      4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db      4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy      4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db      4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy      4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db      4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy      4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db      4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy      4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db      4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy      4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Db      4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Qy      5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
Db      5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
Qy      5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Db      5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Qy      5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Db      5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Qy      5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db      5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 8
US-09-985-637A-1
; Sequence 1, Application US/09985637A
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PR
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA
; FILE REFERENCE: 13587.296
; CURRENT APPLICATION NUMBER: US/09/985,637A
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-985-637A-1

Query Match 99.5%; Score 5246.4; DB 38; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

```
Qy         1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Db         1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Qy        61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db        61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Qy       121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Db       121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Qy       181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db       181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Qy       241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db       241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Qy       301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
```

```
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
```

```
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
```

```
Qy      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db      2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db      2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db      2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db      2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db      2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db      2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db      2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360

Qy      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420

Qy      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

Qy      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy      3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db      3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy      3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db      3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy      4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db      4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy      4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db      4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy      4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db      4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy      4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db      4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259

Qy      4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db      4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy      4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db      4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy      4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db      4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy      4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db      4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy      4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db      4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy      4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db      4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy      4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db      4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy      4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
```

```
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271

Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 9
US-10-244-633-1
; Sequence 1, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 1
; LENGTH: 5300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-1

Query Match 99.5%; Score 5246.4; DB 43; Length 5300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5269; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

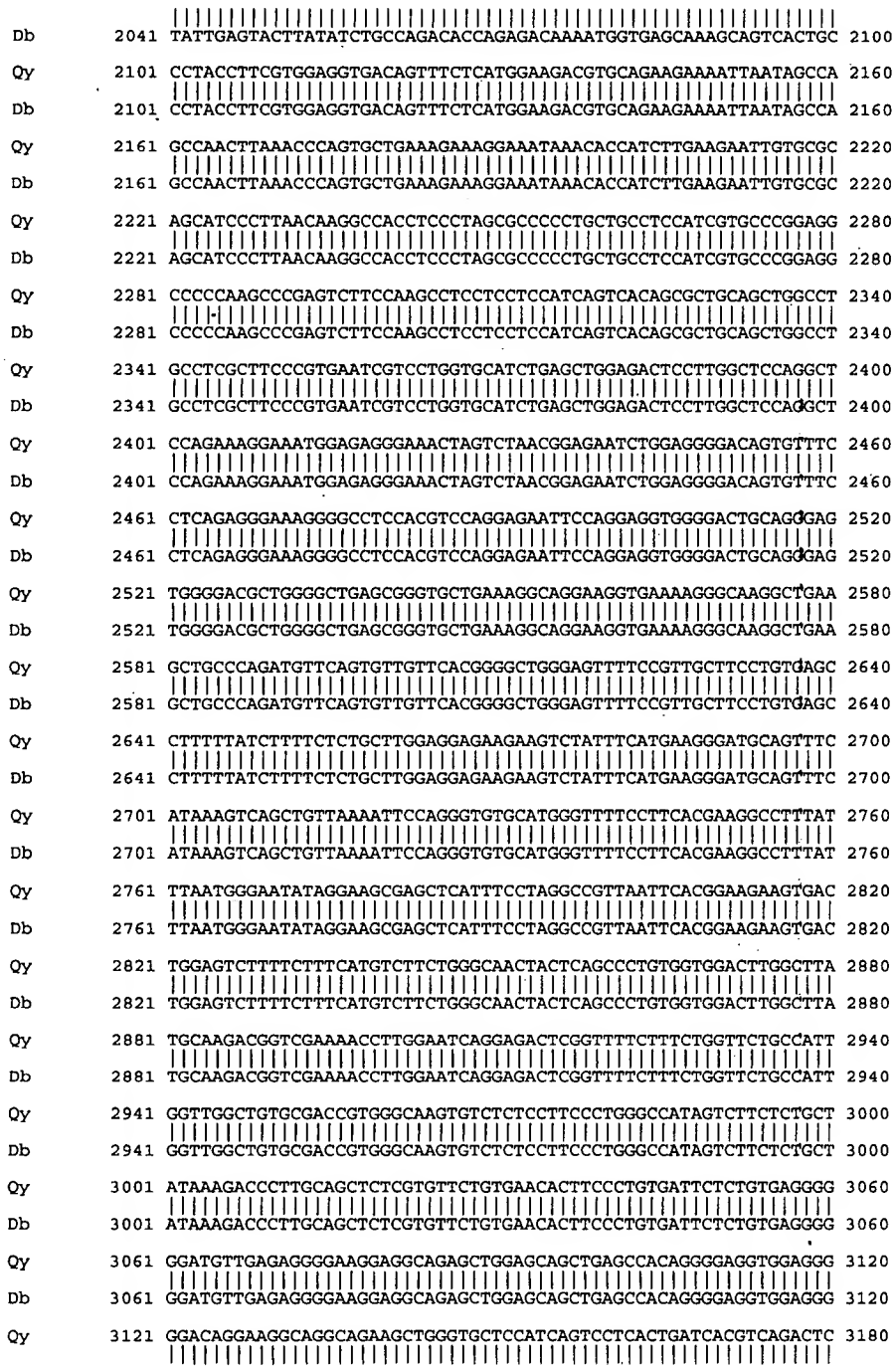
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
```

```
Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100

Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160

Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220

Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280

Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340

Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400

Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460

Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520

Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580

Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640

Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700

Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760

Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820

Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880

Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940

Qy       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000

Qy       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060

Qy       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120

Qy       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180

Qy       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240

Qy       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300

Qy       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db       3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db       3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTTAAAAAGAAACT 5099
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTTAAAAAGAAACT 5099
Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

```
RESULT 10
US-10-741-339-1
; Sequence 1, Application US/10741339
; GENERAL INFORMATION:
;  APPLICANT: Polansky, Jon
;  TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PI
;  TITLE OF INVENTION:  TO DEVELOP GLAUCOMA
;  FILE REFERENCE: 13587.375
;  CURRENT APPLICATION NUMBER: US/10/741,339
;  CURRENT FILING DATE:  2003-12-22
;  PRIOR APPLICATION NUMBER: US 09/985,637
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
```

```
;   LENGTH: 5300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-339-1

  Query Match           99.5%;  Score 5246.4;  DB 61;  Length 5300;
  Best Local Similarity 99.9%;  Pred. No. 0;
  Matches 5269;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620

Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680

Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740

Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800

Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860

Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920

Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980

Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040

Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
```


Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259

```
Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039

Qy       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099

Qy       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
```

RESULT 11
US-10-087-192-1228
; Sequence 1228, Application US/10087192

```
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1228
;   LENGTH: 37252
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-087-192-1228
```

Query Match 99.3%; Score 5232.4; DB 40; Length 37252;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5267; Conservative 0; Mismatches 1; Indels 4; Gaps 3;

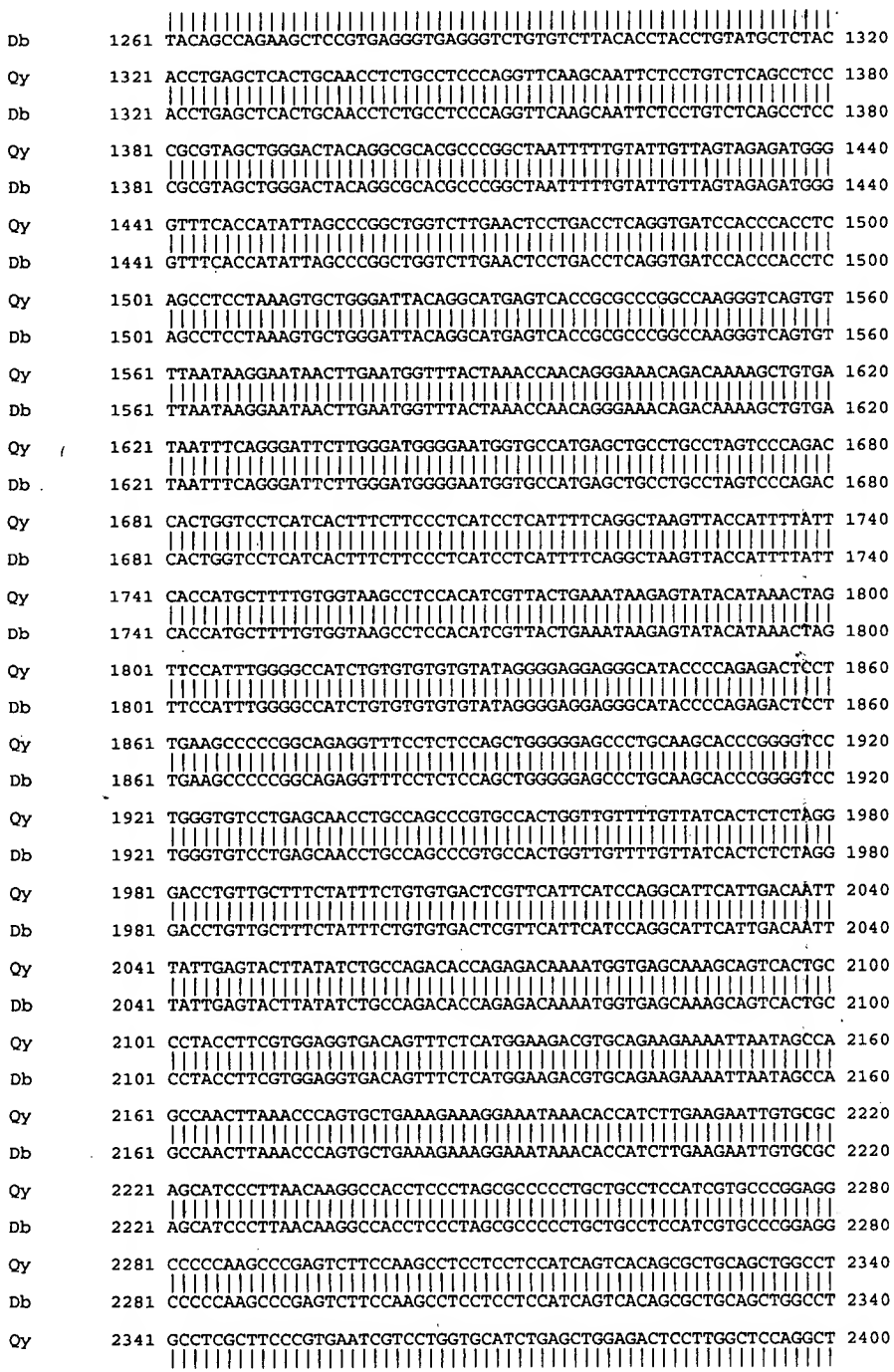
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4731 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 4790

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4791 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 4850

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4851 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 4910

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4911 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 4970

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4971 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 5030

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5031 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 5090

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5091 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 5150

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5151 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 5210

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5211 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 5270

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5271 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 5330

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5331 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 5390

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5391 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 5450

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
```

```
Db       5451 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 5510
Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA  840
Db       5511 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 5570
Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC  900
Db       5571 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 5630
Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG  960
Db       5631 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 5690
Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db       5691 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 5750
Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db       5751 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 5810
Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db       5811 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 5870
Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db       5871 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 5930
Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db       5931 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 5990
Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db       5991 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 6050
Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db       6051 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 6110
Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db       6111 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 6170
Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db       6171 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 6230
Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db       6231 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 6290
Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db       6291 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 6350
Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db       6351 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 6410
Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db       6411 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 6470
Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db       6471 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 6530
Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db       6531 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 6590
Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db       6591 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 6650
Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db       6651 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 6710
Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db       6711 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 6770
Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db       6771 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 6830
Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db       6831 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 6890
Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db       6891 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 6950
Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db       6951 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 7010
Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db       7011 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 7070
Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db       7071 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 7130
Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db       7131 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 7190
Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db       7191 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 7250
Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db       7251 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 7310
Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db       7311 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 7370
Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db       7371 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 7430
Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db       7431 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 7490
Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db       7491 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 7550
Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db       7551 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 7610
Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db       7611 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 7670
```

```
Qy      2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7671 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 7730

Qy      3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7731 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 7790

Qy      3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7791 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 7850

Qy      3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7851 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 7910

Qy      3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7911 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 7970

Qy      3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7971 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 8030

Qy      3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8031 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 8090

Qy      3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8091 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 8150

Qy      3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8151 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 8210

Qy      3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8211 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 8270

Qy      3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8271 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 8330

Qy      3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8331 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 8390

Qy      3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8391 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 8450

Qy      3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8451 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 8510

Qy      3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8511 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 8570

Qy      3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8571 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 8630

Qy      3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| |
Db      8631 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 8690

Qy      3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db      8691 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 8749
```

```
Qy      4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8750 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 8809

Qy      4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8810 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 8869

Qy      4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8870 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 8929

Qy      4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8930 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 8989

Qy      4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8990 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 9049

Qy      4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9050 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 9109

Qy      4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9110 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 9169

Qy      4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9170 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 9229

Qy      4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9230 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 9289

Qy      4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9290 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 9349

Qy      4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9350 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 9409

Qy      4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9410 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 9469

Qy      4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9470 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 9529

Qy      4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9530 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 9589

Qy      4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9590 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 9649

Qy      4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9650 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 9709

Qy      4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 5039
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      9710 GTGTAAGTGTGTGTAC--GTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGAT 9767

Qy      5040 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 5099
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9768 ATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACT 9827

Qy      5100 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 5159
```

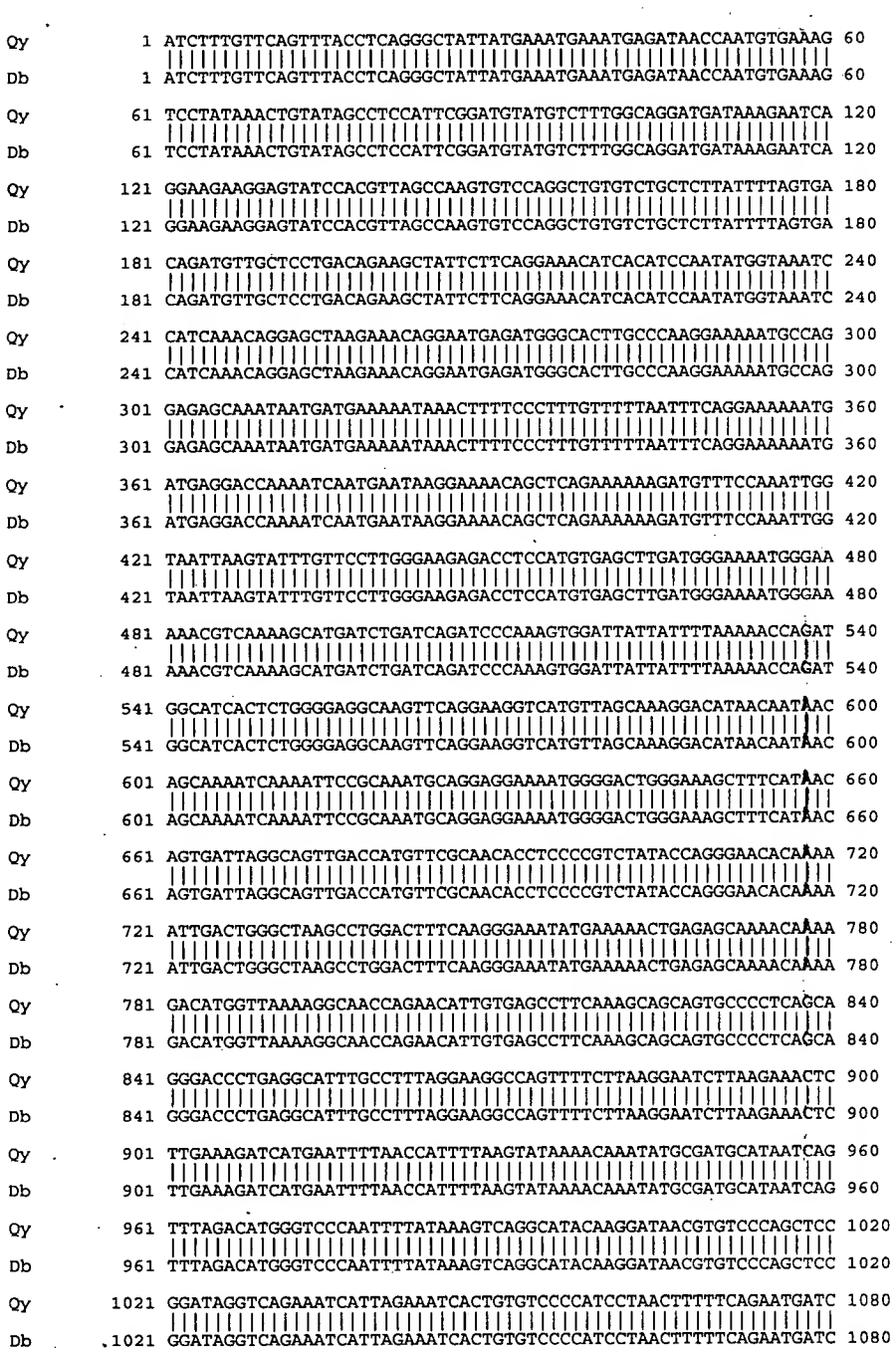
```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9828 CCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCC 9887

Qy       5160 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 5219
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9888 CCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCT 9947

Qy       5220 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9948 GGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 9999


RESULT 12
US-08-938-669-2
; Sequence 2, Application US/08938669
;  GENERAL INFORMATION:
;    APPLICANT:  Nguyen, Thai D.
;    APPLICANT:  Polansky, Jon R.
;    TITLE OF INVENTION:  METHODS FOR THE DIAGNOSIS,
;    TITLE OF INVENTION:  PROGNOSIS AND TREATMENT OF GLAUCOMA AND RELATED DISEASE
;    TITLE OF INVENTION:  S
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howrey & Simon
;      STREET:  1299 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20004-2402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/938,669
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/791,154
;      FILING DATE:  28-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sira, Serge
;      REGISTRATION NUMBER:  39,445
;      REFERENCE/DOCKET NUMBER:  07425-0034
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 383-6857
;      TELEFAX:  202 383-6610
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5304 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-938-669-2

  Query Match             99.1%;  Score 5224.4;  DB 19;  Length 5304;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 5264;  Conservative    0;  Mismatches    6;  Indels    6;  Gaps    3;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
```

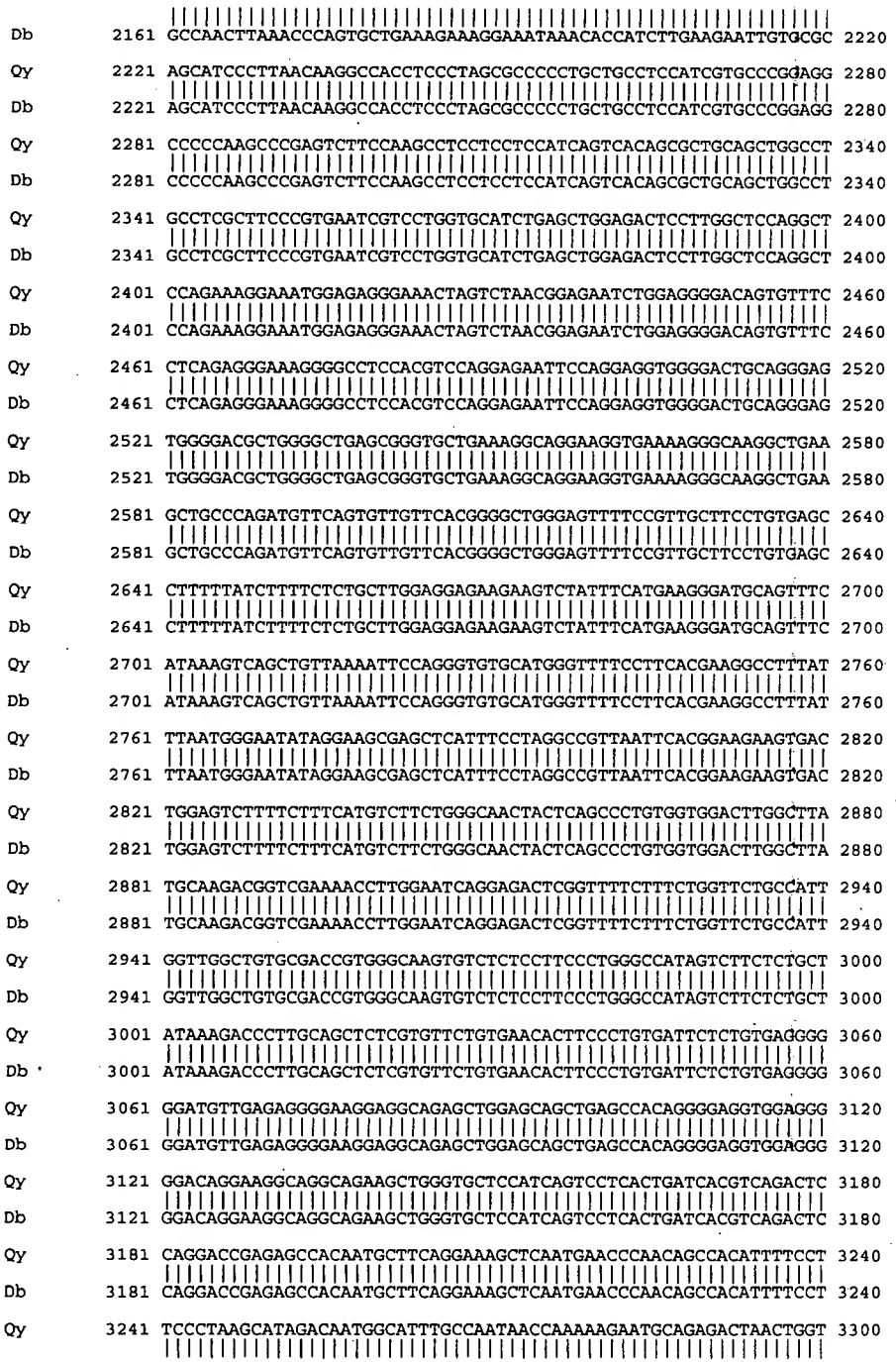

Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480

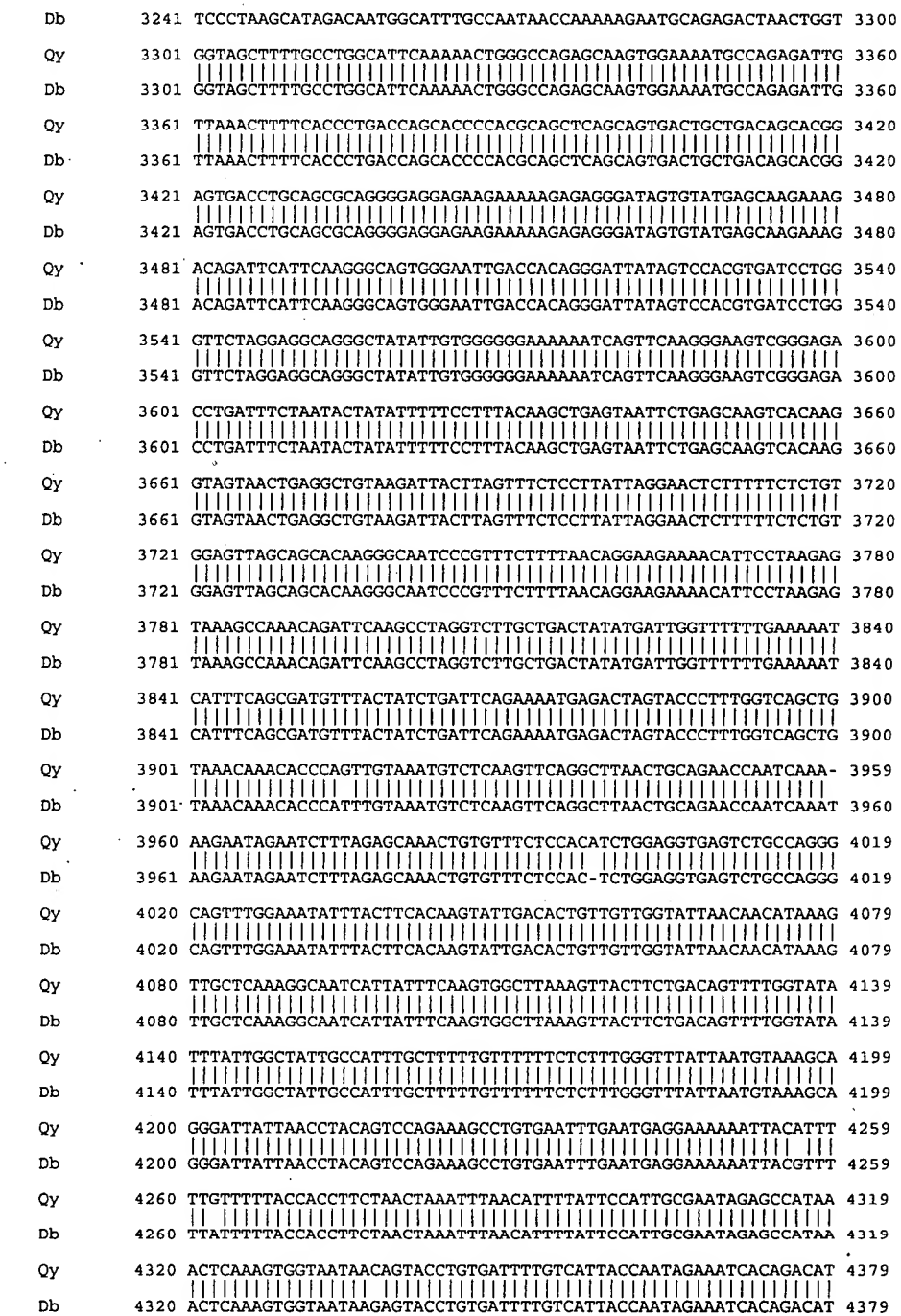
```
Qy       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540

Qy       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600

Qy       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660

Qy       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720

Qy       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780

Qy       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |
Db       3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960

Qy       3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019

Qy       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079

Qy       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139

Qy       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199

Qy       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db       4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259

Qy       4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319

Qy       4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
             ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy       5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099

Qy       5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159

Qy       5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219

Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
```

RESULT 13
US-09-227-881-2
; Sequence 2, Application US/09227881
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis /
; CURRENT APPLICATION NUMBER: US/09/227,881
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: US 08/938,669
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-881-2

Query Match 99.1%; Score 5224.4; DB 22; Length 5304;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;


Qy 1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Db 1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
Qy 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Db 61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
Qy 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Db 121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
Qy 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Db 181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
Qy 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Db 241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
Qy 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Db 301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
Qy 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Db 361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
Qy 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Db 421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
Qy 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Db 481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
Qy 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Db 541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
Qy 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Db 601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
Qy 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Db 661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
Qy 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Db 721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
Qy 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Db 781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db 841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db 901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db 961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db 1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db 1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db 1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db 1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db 1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db 1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db 1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db 1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db 1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db 1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220


Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300


Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259
Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db 4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db 4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379

```
Qy       4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439

Qy       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499

Qy       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559

Qy       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619

Qy       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679

Qy       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739

Qy       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799

Qy       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859

Qy       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919

Qy       4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979

Qy       4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
             ||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db       4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039

Qy       5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099

Qy       5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159

Qy       5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219

Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275
```

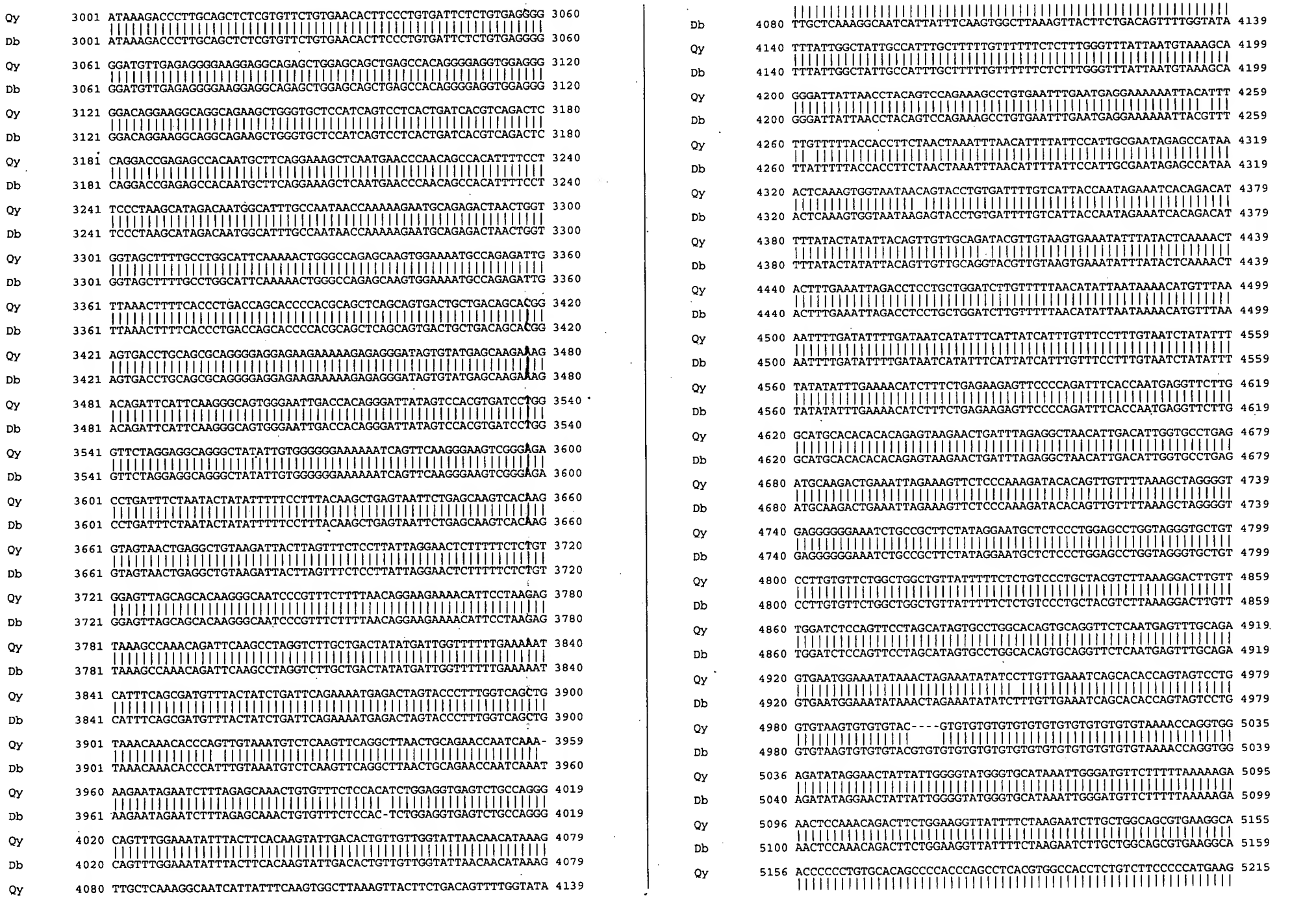
RESULT 14
US-10-244-633-2
; Sequence 2, Application US/10244633
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
; TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
; TITLE OF INVENTION: Disorders
; FILE REFERENCE: 07425.0057.US01
; CURRENT APPLICATION NUMBER: US/10/244,633
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US/09/306,828
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/227,881
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 2
; LENGTH: 5304
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-244-633-2

Query Match 99.1%; Score 5224.4; DB 43; Length 5304;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 5264; Conservative 0; Mismatches 6; Indels 6; Gaps 3;

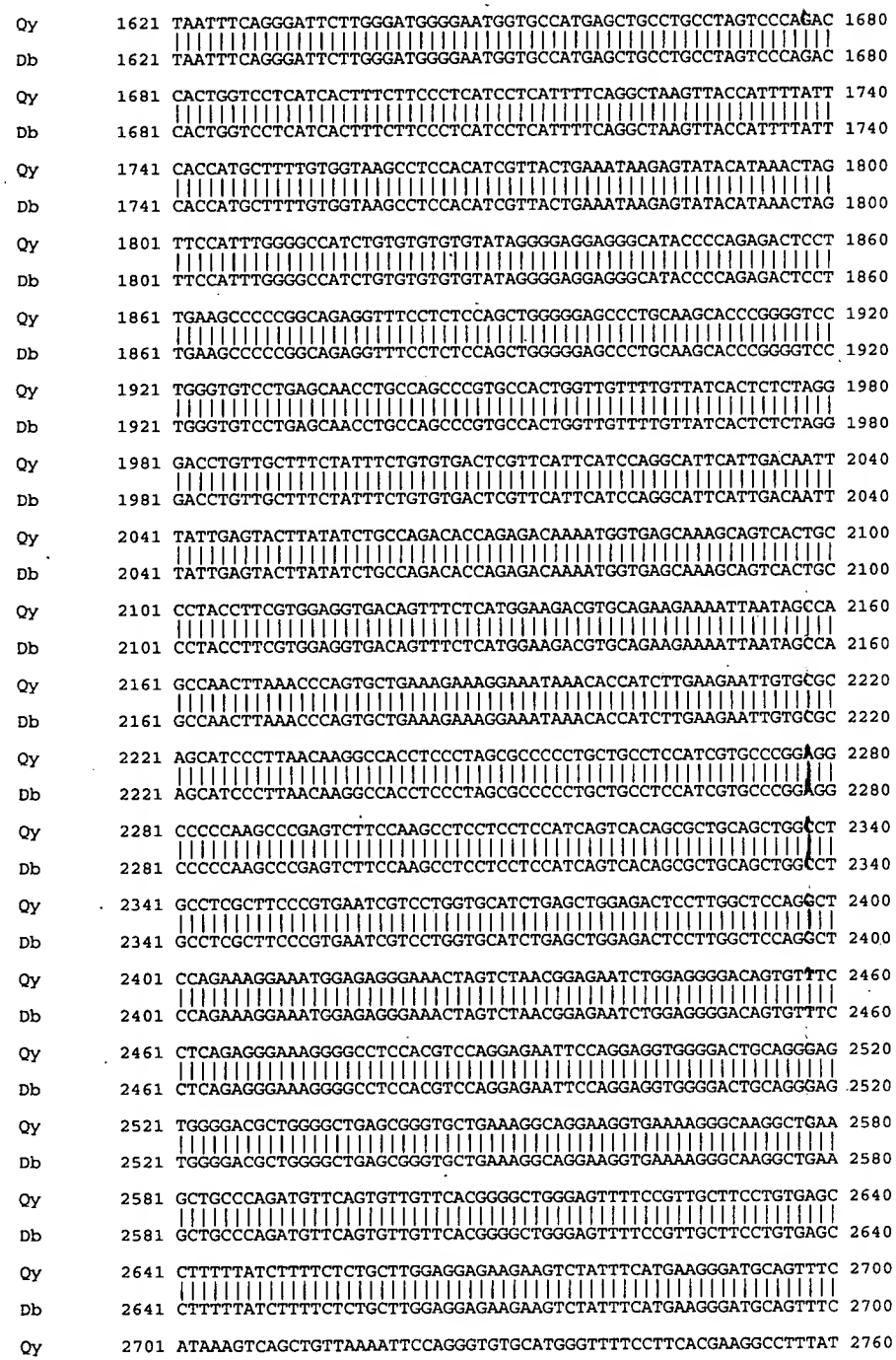
```
Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Db       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440
Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Db       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500
Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Db       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560
Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Db       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
Qy       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db       1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db       1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db       1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db       1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db       1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
```

```
Qy       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db       1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db       1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db       2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db       2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db       2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db       2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db       2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db       2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db       2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db       2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db       2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db       2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db       2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db       2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db       2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db       2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db       2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db       2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
```


Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Db 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840
Qy 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Db 3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
Qy 3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAA- 3959
Db 3901 TAAACAAACACCCATTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAT 3960
Qy 3960 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGG 4019
Db 3961 AAGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCAC-TCTGGAGGTGAGTCTGCCAGGG 4019
Qy 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Db 4020 CAGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAG 4079
Qy 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Db 4080 TTGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATA 4139
Qy 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Db 4140 TTTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCA 4199
Qy 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTT 4259
Db 4200 GGGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACGTTT 4259
Qy 4260 TTGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Db 4260 TTATTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAA 4319
Qy 4320 ACTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Db 4320 ACTCAAAGTGGTAATAAGAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACAT 4379
Qy 4380 TTTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Db 4380 TTTATACTATATTACAGTTGTTGCAGGTACGTTGTAAGTGAAATATTTATACTCAAAACT 4439
Qy 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Db 4440 ACTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAA 4499
Qy 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Db 4500 AATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTT 4559
Qy 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Db 4560 TATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTG 4619
Qy 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Db 4620 GCATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAG 4679
Qy 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Db 4680 ATGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGT 4739
Qy 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Db 4740 GAGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGT 4799
Qy 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Db 4800 CCTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTT 4859
Qy 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Db 4860 TGGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGA 4919
Qy 4920 GTGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Db 4920 GTGAATGGAAATATAAACTAGAAATATATCTTTGTTGAAATCAGCACACCAGTAGTCCTG 4979
Qy 4980 GTGTAAGTGTGTGTAC----GTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5035
Db 4980 GTGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGG 5039
Qy 5036 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5095
Db 5040 AGATATAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGA 5099
Qy 5096 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5155
Db 5100 AACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCA 5159
Qy 5156 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5215

```
Db       5160 ACCCCCCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAG 5219

Qy       5216 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5220 GGCTGGCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5275


RESULT 15
US-60-172-360-23886
; Sequence 23886, Application US/60172360
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
;  FILE REFERENCE: GX-0007 P
;  CURRENT APPLICATION NUMBER: US/60/172,360
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 29838
;  SOFTWARE: PERL Program
; SEQ ID NO 23886
;   LENGTH: 7369
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 223079.1
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1321-1562, 4158-4182, 4874-4912, 4986-5023
;   OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-23886

  Query Match             93.4%;  Score 4925.4;  DB 75;  Length 7369;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 4926;  Conservative    0;  Mismatches  345;  Indels    0;  Gaps    0;

Qy          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATCTTTGTTCAGTTTACCTCAGGGCTATTATGAAATGAAATGAGATAACCAATGTGAAAG 60

Qy         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTATAAACTGTATAGCCTCCATTCGGATGTATGTCTTTGGCAGGATGATAAAGAATCA 120

Qy        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAAGAAGGAGTATCCACGTTAGCCAAGTGTCCAGGCTGTGTCTGCTCTTATTTTAGTGA 180

Qy        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CAGATGTTGCTCCTGACAGAAGCTATTCTTCAGGAAACATCACATCCAATATGGTAAATC 240

Qy        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CATCAAACAGGAGCTAAGAAACAGGAATGAGATGGGCACTTGCCCAAGGAAAAATGCCAG 300

Qy        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAGAGCAAATAATGATGAAAAATAAACTTTTCCCTTTGTTTTTAATTTCAGGAAAAAATG 360

Qy        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGAGGACCAAAATCAATGAATAAGGAAAACAGCTCAGAAAAAAGATGTTTCCAAATTGG 420

Qy        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TAATTAAGTATTTGTTCCTTGGGAAGAGACCTCCATGTGAGCTTGATGGGAAAATGGGAA 480

Qy        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAACGTCAAAAGCATGATCTGATCAGATCCCAAAGTGGATTATTATTTTAAAAACCAGAT 540

Qy        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCATCACTCTGGGGAGGCAAGTTCAGGAAGGTCATGTTAGCAAAGGACATAACAATAAC 600

Qy        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCAAAATCAAAATTCCGCAAATGCAGGAGGAAAATGGGGACTGGGAAAGCTTTCATAAC 660

Qy        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGTGATTAGGCAGTTGACCATGTTCGCAACACCTCCCCGTCTATACCAGGGAACACAAAA 720

Qy        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTGACTGGGCTAAGCCTGGACTTTCAAGGGAAATATGAAAAACTGAGAGCAAAACAAAA 780

Qy        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACATGGTTAAAAGGCAACCAGAACATTGTGAGCCTTCAAAGCAGCAGTGCCCCTCAGCA 840

Qy        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACCCTGAGGCATTTGCCTTTAGGAAGGCCAGTTTTCTTAAGGAATCTTAAGAAACTC 900

Qy        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGAAAGATCATGAATTTTAACCATTTTAAGTATAAAACAAATATGCGATGCATAATCAG 960

Qy        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTAGACATGGGTCCCAATTTTATAAAGTCAGGCATACAAGGATAACGTGTCCCAGCTCC 1020

Qy       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGATAGGTCAGAAATCATTAGAAATCACTGTGTCCCCATCCTAACTTTTTCAGAATGATC 1080

Qy       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTCATAGCCCTCACACACAGGCCCGATGTGTCTGACCTACAACCACATCTACAACCCAA 1140

Qy       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGCCTCAACCATTGTTAACGTGTCATCTCAGTAGGTCCCATTACAAATGCCACCTCCCC 1200

Qy       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCAGCCCATCCCGCTCCACAGGAAGTCTCCCCACTCTAGACTTCTGCATCACGATGT 1260

Qy       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TACAGCCAGAAGCTCCGTGAGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTAC 1320

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380

Db       1321 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1380

Qy       1381 CGCGTAGCTGGGACTACAGGCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGG 1440

Db       1381 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1440

Qy       1441 GTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTC 1500

Db       1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1500

Qy       1501 AGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGT 1560

Db       1501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1560

Qy       1561 TTAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 NNAATAAGGAATAACTTGAATGGTTTACTAAACCAACAGGGAAACAGACAAAAGCTGTGA 1620
```


Qy 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Db 1621 TAATTTCAGGGATTCTTGGGATGGGGAATGGTGCCATGAGCTGCCTGCCTAGTCCCAGAC 1680
Qy 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Db 1681 CACTGGTCCTCATCACTTTCTTCCCTCATCCTCATTTTCAGGCTAAGTTACCATTTTATT 1740
Qy 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Db 1741 CACCATGCTTTTGTGGTAAGCCTCCACATCGTTACTGAAATAAGAGTATACATAAACTAG 1800
Qy 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Db 1801 TTCCATTTGGGGCCATCTGTGTGTGTGTATAGGGGAGGAGGGCATACCCCAGAGACTCCT 1860
Qy 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Db 1861 TGAAGCCCCCGGCAGAGGTTTCCTCTCCAGCTGGGGGAGCCCTGCAAGCACCCGGGGTCC 1920
Qy 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Db 1921 TGGGTGTCCTGAGCAACCTGCCAGCCCGTGCCACTGGTTGTTTTGTTATCACTCTCTAGG 1980
Qy 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Db 1981 GACCTGTTGCTTTCTATTTCTGTGTGACTCGTTCATTCATCCAGGCATTCATTGACAATT 2040
Qy 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Db 2041 TATTGAGTACTTATATCTGCCAGACACCAGAGACAAAATGGTGAGCAAAGCAGTCACTGC 2100
Qy 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Db 2101 CCTACCTTCGTGGAGGTGACAGTTTCTCATGGAAGACGTGCAGAAGAAAATTAATAGCCA 2160
Qy 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Db 2161 GCCAACTTAAACCCAGTGCTGAAAGAAAGGAAATAAACACCATCTTGAAGAATTGTGCGC 2220
Qy 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Db 2221 AGCATCCCTTAACAAGGCCACCTCCCTAGCGCCCCCTGCTGCCTCCATCGTGCCCGGAGG 2280
Qy 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Db 2281 CCCCCAAGCCCGAGTCTTCCAAGCCTCCTCCTCCATCAGTCACAGCGCTGCAGCTGGCCT 2340
Qy 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Db 2341 GCCTCGCTTCCCGTGAATCGTCCTGGTGCATCTGAGCTGGAGACTCCTTGGCTCCAGGCT 2400
Qy 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Db 2401 CCAGAAAGGAAATGGAGAGGGAAACTAGTCTAACGGAGAATCTGGAGGGGACAGTGTTTC 2460
Qy 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Db 2461 CTCAGAGGGAAAGGGGCCTCCACGTCCAGGAGAATTCCAGGAGGTGGGGACTGCAGGGAG 2520
Qy 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Db 2521 TGGGGACGCTGGGGCTGAGCGGGTGCTGAAAGGCAGGAAGGTGAAAAGGGCAAGGCTGAA 2580
Qy 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Db 2581 GCTGCCCAGATGTTCAGTGTTGTTCACGGGGCTGGGAGTTTTCCGTTGCTTCCTGTGAGC 2640
Qy 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Db 2641 CTTTTTATCTTTTCTCTGCTTGGAGGAGAAGAAGTCTATTTCATGAAGGGATGCAGTTTC 2700
Qy 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Db 2701 ATAAAGTCAGCTGTTAAAATTCCAGGGTGTGCATGGGTTTTCCTTCACGAAGGCCTTTAT 2760
Qy 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Db 2761 TTAATGGGAATATAGGAAGCGAGCTCATTTCCTAGGCCGTTAATTCACGGAAGAAGTGAC 2820
Qy 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Db 2821 TGGAGTCTTTTCTTTCATGTCTTCTGGGCAACTACTCAGCCCTGTGGTGGACTTGGCTTA 2880
Qy 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Db 2881 TGCAAGACGGTCGAAAACCTTGGAATCAGGAGACTCGGTTTTCTTTCTGGTTCTGCCATT 2940
Qy 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Db 2941 GGTTGGCTGTGCGACCGTGGGCAAGTGTCTCTCCTTCCCTGGGCCATAGTCTTCTCTGCT 3000
Qy 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Db 3001 ATAAAGACCCTTGCAGCTCTCGTGTTCTGTGAACACTTCCCTGTGATTCTCTGTGAGGGG 3060
Qy 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Db 3061 GGATGTTGAGAGGGGAAGGAGGCAGAGCTGGAGCAGCTGAGCCACAGGGGAGGTGGAGGG 3120
Qy 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Db 3121 GGACAGGAAGGCAGGCAGAAGCTGGGTGCTCCATCAGTCCTCACTGATCACGTCAGACTC 3180
Qy 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Db 3181 CAGGACCGAGAGCCACAATGCTTCAGGAAAGCTCAATGAACCCAACAGCCACATTTTCCT 3240
Qy 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Db 3241 TCCCTAAGCATAGACAATGGCATTTGCCAATAACCAAAAAGAATGCAGAGACTAACTGGT 3300
Qy 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Db 3301 GGTAGCTTTTGCCTGGCATTCAAAAACTGGGCCAGAGCAAGTGGAAAATGCCAGAGATTG 3360
Qy 3361 TTAAACTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Db 3361 TTAAACTTTCACCCTGACCAGCACCCCACGCAGCTCAGCAGTGACTGCTGACAGCACGG 3420
Qy 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Db 3421 AGTGACCTGCAGCGCAGGGGAGGAGAAGAAAAAGAGAGGGATAGTGTATGAGCAAGAAAG 3480
Qy 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Db 3481 ACAGATTCATTCAAGGGCAGTGGGAATTGACCACAGGGATTATAGTCCACGTGATCCTGG 3540
Qy 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Db 3541 GTTCTAGGAGGCAGGGCTATATTGTGGGGGGAAAAAATCAGTTCAAGGGAAGTCGGGAGA 3600
Qy 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Db 3601 CCTGATTTCTAATACTATATTTTTCCTTTACAAGCTGAGTAATTCTGAGCAAGTCACAAG 3660
Qy 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Db 3661 GTAGTAACTGAGGCTGTAAGATTACTTAGTTTCTCCTTATTAGGAACTCTTTTTCTCTGT 3720
Qy 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Db 3721 GGAGTTAGCAGCACAAGGGCAATCCCGTTTCTTTTAACAGGAAGAAAACATTCCTAAGAG 3780
Qy 3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

```
Db       3781 TAAAGCCAAACAGATTCAAGCCTAGGTCTTGCTGACTATATGATTGGTTTTTTGAAAAAT 3840

Qy       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CATTTCAGCGATGTTTACTATCTGATTCAGAAAATGAGACTAGTACCCTTTGGTCAGCTG 3900

Qy       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 TAAACAAACACCCAGTTGTAAATGTCTCAAGTTCAGGCTTAACTGCAGAACCAATCAAAA 3960

Qy       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 AGAATAGAATCTTTAGAGCAAACTGTGTTTCTCCACATCTGGAGGTGAGTCTGCCAGGGC 4020

Qy       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 AGTTTGGAAATATTTACTTCACAAGTATTGACACTGTTGTTGGTATTAACAACATAAAGT 4080

Qy       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 TGCTCAAAGGCAATCATTATTTCAAGTGGCTTAAAGTTACTTCTGACAGTTTTGGTATAT 4140

Qy       4141 TTATTGGCTATTGCCATTTGCTTTTTGTTTTTTCTCTTTGGGTTTATTAATGTAAAGCAG 4200
             ||||||||||||||||                ||||||||||||||||||||||||||||||
Db       4141 TTATTGGCTATTGCCATNNNNNNNNNNNNNNNNNNNNNNNNNTTTATTAATGTAAAGCAG 4200

Qy       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 GGATTATTAACCTACAGTCCAGAAAGCCTGTGAATTTGAATGAGGAAAAAATTACATTTT 4260

Qy       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 TGTTTTTACCACCTTCTAACTAAATTTAACATTTTATTCCATTGCGAATAGAGCCATAAA 4320

Qy       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 CTCAAAGTGGTAATAACAGTACCTGTGATTTTGTCATTACCAATAGAAATCACAGACATT 4380

Qy       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 TTATACTATATTACAGTTGTTGCAGATACGTTGTAAGTGAAATATTTATACTCAAAACTA 4440

Qy       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 CTTTGAAATTAGACCTCCTGCTGGATCTTGTTTTTAACATATTAATAAAACATGTTTAAA 4500

Qy       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 ATTTTGATATTTTGATAATCATATTTCATTATCATTTGTTTCCTTTGTAATCTATATTTT 4560

Qy       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 ATATATTTGAAAACATCTTTCTGAGAAGAGTTCCCCAGATTTCACCAATGAGGTTCTTGG 4620

Qy       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 CATGCACACACACAGAGTAAGAACTGATTTAGAGGCTAACATTGACATTGGTGCCTGAGA 4680

Qy       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 TGCAAGACTGAAATTAGAAAGTTCTCCCAAAGATACACAGTTGTTTTAAAGCTAGGGGTG 4740

Qy       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 AGGGGGGAAATCTGCCGCTTCTATAGGAATGCTCTCCCTGGAGCCTGGTAGGGTGCTGTC 4800

Qy       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 CTTGTGTTCTGGCTGGCTGTTATTTTTCTCTGTCCCTGCTACGTCTTAAAGGACTTGTTT 4860

Qy       4861 GGATCTCCAGTTCCTAGCATAGTGCCTGGCACAGTGCAGGTTCTCAATGAGTTTGCAGAG 4920
             ||||||||||||                                ||||||||
Db       4861 GGATCTCCAGTTCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGCAGAG 4920

Qy       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 TGAATGGAAATATAAACTAGAAATATATCCTTGTTGAAATCAGCACACCAGTAGTCCTGG 4980

Qy       4981 TGTAAGTGTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTAAAACCAGGTGGAGATA 5040
             |||||                                        ||||||||||||||||
Db       4981 TGTAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAACCAGGTGGAGATA 5040

Qy       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TAGGAACTATTATTGGGGTATGGGTGCATAAATTGGGATGTTCTTTTTAAAAAGAAACTC 5100

Qy       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 CAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGGCAACCCC 5160

Qy       5161 CCTGTGCACAGCCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 CCTGTGCACAGCCCCACCCAGCCTCACGTGGCCACCTCTGTCTTCCCCCATGAAGGGCTG 5220

Qy       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 5271
             |||||||||||||||||||||||||||||| ||||||||||||||||||
Db       5221 GCTCCCCAGTATATATAAACCTCTCTGGAGCTCAGGCATGAGCCAGCAAGG 5271
```

Search completed: January 26, 2006, 09:13:42
Job time : 17364 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 26, 2006, 03:03:01 ; Search time 758 Seconds
(without alignments)
12735.951 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atctttgttcagtttacctc.....tcgggcatgagccagcaagg 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3416786 seqs, 915751376 residues

Total number of hits satisfying chosen parameters: 6833572

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.17Jan05:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.new:*
9: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq1:*
11: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2:*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		184.8	3.5	1000	11	US-11-266-748A-198985	Sequence 198985,
2	c	184.4	3.5	1000	11	US-11-266-748A-224089	Sequence 224089,
3	c	184.4	3.5	1770	11	US-11-266-748A-26905	Sequence 26905, A
4		184.2	3.5	1000	11	US-11-266-748A-195297	Sequence 195297,
5		183.6	3.5	17691	6	US-10-868-184C-6721	Sequence 6721, Ap
6		183.6	3.5	17691	7	US-10-868-184C-6721	Sequence 6721, Ap
7		182.4	3.5	515	11	US-11-266-748A-212844	Sequence 212844,
8	c	182.4	3.5	515	11	US-11-266-748A-236144	Sequence 236144,
9		180.8	3.4	101500	11	US-11-266-748A-61740	Sequence 61740, A
10		180.6	3.4	39729	11	US-11-214-063A-1285	Sequence 1285, Ap
11		179.4	3.4	10948	11	US-11-214-063A-1715	Sequence 1715, Ap
12	c	179.2	3.4	6708	6	US-10-868-184C-6360	Sequence 6360, Ap
13	c	179.2	3.4	6708	6	US-10-868-184C-11267	Sequence 11267, A
14	c	179.2	3.4	6708	7	US-10-868-184C-6360	Sequence 6360, Ap
15	c	179.2	3.4	6708	7	US-10-868-184C-11267	Sequence 11267, A
16	c	179.2	3.4	189450	1	PCT-US05-10912-6	Sequence 6, Appli
17	c	179.2	3.4	495475	11	US-11-266-748A-28223	Sequence 28223, A
18		178.6	3.4	124048	11	US-11-266-748A-59707	Sequence 59707, A
19	c	177.8	3.4	155379	11	US-11-266-748A-24170	Sequence 24170, A
20	c	177.8	3.4	155379	11	US-11-266-748A-59410	Sequence 59410, A
21		177.8	3.4	227968	11	US-11-266-748A-60135	Sequence 60135, A
22		177.6	3.4	128978	11	US-11-266-748A-61436	Sequence 61436, A
23	c	176.8	3.4	53332	6	US-10-786-065-3	Sequence 3, Appli
24	c	176.8	3.4	53332	7	US-10-786-065-3	Sequence 3, Appli
25	c	176.6	3.4	1173	6	US-10-461-673-4221	Sequence 4221, Ap
26	c	176.6	3.4	1173	8	US-10-461-673-4221	Sequence 4221, Ap
27	c	176	3.3	1400	6	US-10-868-184C-7974	Sequence 7974, Ap
28	c	176	3.3	1400	7	US-10-868-184C-7974	Sequence 7974, Ap
29	c	176	3.3	2213	6	US-10-868-184C-7973	Sequence 7973, Ap
30	c	176	3.3	2213	7	US-10-868-184C-7973	Sequence 7973, Ap
31		176	3.3	164429	11	US-11-266-748A-22662	Sequence 22662, A
32		175.6	3.3	1000	11	US-11-266-748A-196932	Sequence 196932,
33		175.6	3.3	3143	11	US-11-266-748A-28298	Sequence 28298, A
34		175.4	3.3	6110	11	US-11-266-748A-24483	Sequence 24483, A
35		175.4	3.3	100096	11	US-11-266-748A-59715	Sequence 59715, A
36		175.2	3.3	65854	6	US-10-868-184C-12628	Sequence 12628, A
37	c	175.2	3.3	65854	6	US-10-868-184C-13035	Sequence 13035, A
38		175.2	3.3	65854	7	US-10-868-184C-12628	Sequence 12628, A
39	c	175.2	3.3	65854	7	US-10-868-184C-13035	Sequence 13035, A
40	c	175.2	3.3	822900	11	US-11-214-063A-1393	Sequence 1393, Ap
41		175	3.3	1000	11	US-11-266-748A-197285	Sequence 197285,
42		175	3.3	2297	6	US-10-276-817B-3434	Sequence 3434, Ap
43		175	3.3	2297	7	US-10-276-817B-3434	Sequence 3434, Ap
44	c	175	3.3	6615	11	US-11-266-748A-30008	Sequence 30008, A
45	c	175	3.3	6639	11	US-11-266-748A-30006	Sequence 30006, A

ALIGNMENTS

RESULT 1
US-11-266-748A-198985
; Sequence 198985, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 198985
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-198985

Query Match 3.5%; Score 184.8; DB 11; Length 1000;
Best Local Similarity 78.2%; Pred. No. 5.3e-36;
Matches 222; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
Db 578 GAGTCTCGCTCTGTTACCCATGCTGGAGTGCAGTGGCGCTATCTCAGCTCACTGCAACCT 637

```
Qy       1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
Db        638 CCGCCTCCCGGGTTCAAGCAATTCTCCTGCCTTAGCTTCCTGAGTAGCTGGGATTACAGG 697

Qy       1401 CGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGG 1460
Db        698 CTCATGCCAATTTAATTTTTGTATTTTTAGTAGAGTCGGGGTTTCGCTATGTTGGCCAGG 757

Qy       1461 CTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGA 1520
Db        758 CTGGTCTTGAACTTCTGACCTCAGGTGATCCACCCGCCTCAGCCTCCCAAAGTGCTGGGA 817

Qy       1521 TTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAA 1564
Db        818 TTACAGGCATGAGCCACCACACCCGGCCAGTGAAGGGTCTTTTA 861
```

RESULT 2
US-11-266-748A-224089/c
; Sequence 224089, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 224089
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-224089

Query Match 3.5%; Score 184.4; DB 11; Length 1000;
Best Local Similarity 81.0%; Pred. No. 6.7e-36;
Matches 230; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

```
Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db        938 ATCTCAGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCGATTCCCCTGCCTCAGCCTCC 879

Qy       1381 CGCGTAGCTGGGACTACAGGCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
Db        878 CGAGCAGCTGGGACTACAGGCGCCCGACACCACGCCCGGCTAATTTTTGTATTTTTAGTA 819

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
Db        818 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCCGACCTCAGGTGATCTG 759

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
Db        758 CCCGCCTCGGCCTCCCAAAGTGGTGGGATTACAGGCATGAGCCACCGCATCCGGCCAGAT 699

Qy       1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAACCAA 1596
Db        698 TTCAGGTGCTTTTAAAAAGTAACTGAAATTTTATTTTTACTTAA 655
```

RESULT 3
US-11-266-748A-26905/c
; Sequence 26905, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26905
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-26905

Query Match 3.5%; Score 184.4; DB 11; Length 1770;
Best Local Similarity 81.0%; Pred. No. 8.4e-36;
Matches 230; Conservative 0; Mismatches 46; Indels 8; Gaps 1;

```
Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
Db       1708 ATCTCAGCTCACTGCAACCTCCGCCTCCCAGGTTCAAGCGATTCCCCTGCCTCAGCCTCC 1649

Qy       1381 CGCGTAGCTGGGACTACAGGCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
Db       1648 CGAGCAGCTGGGACTACAGGCGCCCGACACCACGCCCGGCTAATTTTTGTATTTTTAGTA 1589

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
Db       1588 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCCGACCTCAGGTGATCTG 1529

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
Db       1528 CCCGCCTCGGCCTCCCAAAGTGGTGGGATTACAGGCATGAGCCACCGCATCCGGCCAGAT 1469

Qy       1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACTAAACCAA 1596
Db       1468 TTCAGGTGCTTTTAAAAAGTAACTGAAATTTTATTTTTACTTAA 1425
```

RESULT 4
US-11-266-748A-195297
; Sequence 195297, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl

```
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 195297
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-195297

  Query Match             3.5%;  Score 184.2;  DB 11;  Length 1000;
  Best Local Similarity   72.9%;  Pred. No. 7.5e-36;
  Matches  237;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy       1280 AGGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACC 1339
             || ||   | |||||  |  |  |     | |    |   | || | ||||||||||||
Db         58 AGAGTCTTGTTCTGTCACCCAGGCTGGGGTACAGTGGCGTGATCTCAACTCACTGCAACC 117

Qy       1340 TCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAG 1399
             | ||||||||||||||||| ||||||    |||||||| ||  ||||||||||||||||
Db         118 TGTGCCTCCCAGGTTCAAGCGATTCTCACTCCTCAGCCTTCCAAGTAGCTGGGACTACAG 177

Qy       1400 GCGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCG 1459
             | ||||||| |||||||||||||| |||||||||| || ||||| ||||| | |||
Db         178 GTGCACGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGGAGTTTCCCCATACTGGCCAA 237

Qy       1460 GCTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGG 1519
             ||||||  |||||||||||||||||| |||||||||  |||| ||||||  ||||||  ||||
Db         238 GCTGGTTTTGAACTCCTGACCTCAAGTGATCCACCAGCCTCGGCCTCCCAAAGTGTTGGG 297

Qy       1520 ATTACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
             |||||||||||||| ||   || ||| ||||||     |    ||||  || | ||||    |
Db         298 ATTACAGGCATGAGCCAATGCACCCAGCCAAGTTCTGGGTCTTAACAATGTATAATGCCA 357

Qy       1580 ATGGTTTACTAAACCAACAGGGAAA 1604
                | |  ||  |   | ||   |||
Db         358 TGGATCCACACATGTAGCAACAAAA 382


RESULT 5
US-10-868-184C-6721
; Sequence 6721, Application US/10868184C
; GENERAL INFORMATION:
;  APPLICANT: Rosen, et. al
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS805
;  CURRENT APPLICATION NUMBER: US/10/868,184C
;  CURRENT FILING DATE:  2004-06-16
;  PRIOR APPLICATION NUMBER: 60/278,650
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/833,245
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US01/11988
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US00/06043
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06012
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06058
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06044
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06059
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06042
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06014
;  PRIOR FILING DATE: 2000-03-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13046
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6721
;   LENGTH: 17691
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-868-184C-6721

  Query Match             3.5%;  Score 183.6;  DB 6;  Length 17691;
  Best Local Similarity   78.2%;  Pred. No. 3.4e-35;
  Matches  233;  Conservative    0;  Mismatches   64;  Indels    1;  Gaps    1;

Qy       1283 GTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCT 1342
             ||   | |||||  |  |  |     || |    |   | || ||||||||||||||||
Db      14938 GTCTCGCTCTGTCGCCCAGGCAGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCT 14997

Qy       1343 GCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG 1402
             |||||||||||||||||||||||||||||| |||||||||| ||||| |||| |||||| |
Db      14998 GCCTCCCAGGTTCAAGCAATTCTCCTGTTTCAGCCTCCCGAGTAGCAGGGATTACAGGTG 15057

Qy       1403 CACGCCCGGCTAA-TTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461
              ||||| ||||| |||||||||| |||||||||  |||||||||||| || ||| |||
Db      15058 TGCGCCCAGCTAATTTTTTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGC 15117

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
             |||||||||||||||||||| |||||||||| ||||  ||||| ||||||||||||||
Db      15118 TGGTCTTGAACTCCTGACCTCAAGTGATCCACCCTCCTCCACCTCCGAAAGTGCTGGGAT 15177

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
             || ||||||||| ||||| || ||||||  || |    |||||     || |  |  ||
Db      15178 TATAGGCATGAGCCACCGTGCTCGGCCAGAGGCCTTCTTTTAAGTGTGACTTCCAAGA 15235


RESULT 6
US-10-868-184C-6721
; Sequence 6721, Application US/10868184C
; GENERAL INFORMATION:
;  APPLICANT: Rosen, et. al
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS805
;  CURRENT APPLICATION NUMBER: US/10/868,184C
;  CURRENT FILING DATE:  2004-06-16
;  PRIOR APPLICATION NUMBER: 60/278,650
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/833,245
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US01/11988
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US00/06043
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06012
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06058
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06044
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06059
;  PRIOR FILING DATE: 2000-03-09
```

```
;  PRIOR APPLICATION NUMBER: PCT/US00/06042
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06014
;  PRIOR FILING DATE: 2000-03-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13046
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6721
;    LENGTH: 17691
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-868-184C-6721

  Query Match             3.5%;  Score 183.6;  DB 7;  Length 17691;
  Best Local Similarity   78.2%;  Pred. No. 3.4e-35;
  Matches  233;  Conservative    0;  Mismatches   64;  Indels    1;  Gaps    1;

Qy       1283 GTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCT 1342
              ||   | |||||  |  |  |    || |     |  || ||||||||||||||||||
Db      14938 GTCTCGCTCTGTCGCCCAGGCAGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCT 14997

Qy       1343 GCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG 1402
              |||||||||||||||||||||||||||| |||||||||| ||||| |||| |||||| |
Db      14998 GCCTCCCAGGTTCAAGCAATTCTCCTGTTTCAGCCTCCCGAGTAGCAGGGATTACAGGTG 15057

Qy       1403 CACGCCCGGCTAA-TTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461
                ||||| ||||| |||||||||| |||||||||  |||||||||||  || ||| |||
Db      15058 TGCGCCCAGCTAATTTTTTGTATTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGC 15117

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
              |||||||||||||||||||| |||||||||| ||||  ||||| ||||||||||||||
Db      15118 TGGTCTTGAACTCCTGACCTCAAGTGATCCACCCTCCTCCACCTCCGAAAGTGCTGGGAT 15177

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
              || ||||||||| ||||| || ||||||  || |    |||||    || |  | ||
Db      15178 TATAGGCATGAGCCACCGTGCTCGGCCAGAGGCCTTCTTTTAAGTGTGACTTCCAAGA 15235


RESULT 7
US-11-266-748A-212844
; Sequence 212844, Application US/11266748A
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 212844
;    LENGTH: 515
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-266-748A-212844

  Query Match             3.5%;  Score 182.4;  DB 11;  Length 515;
  Best Local Similarity   86.4%;  Pred. No. 1.6e-35;
  Matches  216;  Conservative    0;  Mismatches   26;  Indels    8;  Gaps    1;

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              | || ||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||
Db         46 ATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGTCTCAGCCTCC 105

Qy       1381 CGCGTAGCTGGGACTACAGGCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
              |  |||||||||| ||||||||        |||||||||||||||||||||| ||||||
Db         106 CAAGTAGCTGGGATTACAGGCGCACACCACCACGCCCGGCTAATTTTTGTATTTTTAGTA 165

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
              |||||||||||||||||  || ||| |||||||| ||||||||||||||||||||||||||
Db         166 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCA 225

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
              |||||||| |||||| |||||||||||||||||||| || | ||| |||||| ||| |
Db         226 CCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCCTGGGCCACTGCGCCCAGCCTAAT 285

Qy       1553 GTCAGTGTTT 1562
              |  || |||
Db         286 TTTTGTATTT 295


RESULT 8
US-11-266-748A-236144/c
; Sequence 236144, Application US/11266748A
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 236144
;    LENGTH: 515
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-266-748A-236144

  Query Match             3.5%;  Score 182.4;  DB 11;  Length 515;
  Best Local Similarity   86.4%;  Pred. No. 1.6e-35;
  Matches  216;  Conservative    0;  Mismatches   26;  Indels    8;  Gaps    1;

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              | || ||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||
Db         470 ATCTCAGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGTCTCAGCCTCC 411

Qy       1381 CGCGTAGCTGGGACTACAGGCG--------CACGCCCGGCTAATTTTTGTATTGTTAGTA 1432
              |  |||||||||| ||||||||        |||||||||||||||||||||| ||||||
Db         410 CAAGTAGCTGGGATTACAGGCGCACACCACCACGCCCGGCTAATTTTTGTATTTTTAGTA 351
```

```
Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
             ||||||||||||||||||| || ||| |||||||||| ||||||||||||||||||||||||
Db        350 GAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCA 291

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
             |||||||| |||||| ||||||||||||||||||| || | ||| |||||| ||| |
Db        290 CCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCCTGGGCCACTGCGCCCAGCCTAAT 231

Qy       1553 GTCAGTGTTT 1562
                |  || |||
Db        230 TTTTGTATTT 221
```

RESULT 9
US-11-266-748A-61740
; Sequence 61740, Application US/11266748A
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61740
; LENGTH: 101500
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61740

Query Match 3.4%; Score 180.8; DB 11; Length 101500;
Best Local Similarity 79.0%; Pred. No. 3.4e-34;
Matches 215; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```
Qy       1281 GGGTGAGGGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCT 1340
             | ||   | |||||  |  |  |    || |     |   | ||  ||||| ||||||||
Db      76041 GAGTCTCGCTCTGTTGCCCAGGCTAGAGTGCAATGGCACGATCTTGGCTCATTGCAACCT 76100

Qy       1341 CTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGG 1400
             | ||||||||||||||||| || |||||| ||||| | |||  |||||||||| ||||||
Db      76101 CGGCCTCCCAGGTTCAAGCGATCCTCCTGCCTCAGTCACCCTAGTAGCTGGGATTACAGG 76160

Qy       1401 CGCACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGG 1460
             |   | ||||||||||||||||||  |||||||||  | ||||||||||| || ||| ||
Db      76161 CATGCACCCGGCTAATTTTTGTATTTATAGTAGAGACAGAGTTTCACCATGTTGGCCAGG 76220

Qy       1461 CTGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGA 1520
             ||||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      76221 CTGGTCTCGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGA 76280

Qy       1521 TTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
             |||||||| |||| ||| | |||||||| | |
Db      76281 TTACAGGCGTGAGCCACTGTGCCCGGCCCAAG 76312
```

RESULT 10
US-11-214-063A-1285
; Sequence 1285, Application US/11214063A
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/11/214,063A
; CURRENT FILING DATE: 2005-08-30
; PRIOR APPLICATION NUMBER: US/10/292,798
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1285
; LENGTH: 39729
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(39729)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(409)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1705)..(1966)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3861)..(4281)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6128)..(6513)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13450)..(13658)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15064)..(15254)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15941)..(16150)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20045)..(20170)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22124)..(22422)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22512)..(22683)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23437)..(23604)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (24073)..(24309)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27352)..(27646)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (28263)..(28408)
; FEATURE:

```
;   NAME/KEY: CDS
;   LOCATION: (28910)..(29146)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (30241)..(30380)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (36370)..(36640)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (36749)..(36992)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39268)..(39529)
US-11-214-063A-1285

  Query Match             3.4%;  Score 180.6;  DB 11;  Length 39729;
  Best Local Similarity   81.2%;  Pred. No. 2.6e-34;
  Matches  225;  Conservative    0;  Mismatches   44;  Indels    8;  Gaps    1;

Qy       1321 ACCTGAGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCC 1380
              | ||  |||||||||||||||||||||  |||||||  | |||||||||| ||||||||||
Db      24907 ATCTCGGCTCACTGCAACCTCTGCCTCCAGGGTTCAATCGATTCTCCTGCCTCAGCCTCC 24966

Qy       1381 CGCGTAGCTGGGACTACAGGCGCAC--------GCCCGGCTAATTTTTGTATTGTTAGTA 1432
              || ||||||||||  |||||  || |        ||| ||||||||||||||| ||||||
Db      24967 CGAGTAGCTGGGATGACAGGTGCGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTA 25026

Qy       1433 GAGATGGGGTTTCACCATATTAGCCCGGCTGGTCTTGAACTCCTGACCTCAGGTGATCCA 1492
              ||||  |||||||||||| || ||| |||||||||| ||||||||||||||||||||||||
Db      25027 GAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCCG 25086

Qy       1493 CCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGGCATGAGTCACCGCGCCCGGCCAAGG 1552
              ||| |||||||||||  |||||||||||||||||||||||||| |||||||||||||   |
Db      25087 CCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGCGCCCGGCCTGAG 25146

Qy       1553 GTCAGTGTTTAATAAGGAATAACTTGAATGGTTTACT 1589
                |     ||||  |||||    ||||  |||||  ||
Db      25147 TTTTCCTTTTATGAAGGACCTGCTTGGTTGGTTGCCT 25183


RESULT 11
US-11-214-063A-1715
; Sequence 1715, Application US/11214063A
; GENERAL INFORMATION:
;  APPLICANT: SUWA, MAKIKO
;  APPLICANT:  ASAI, KIYOSHI
;  APPLICANT:  AKIYAMA, YUTAKA
;  APPLICANT:  ABURATANI, HIROYUKI
;  TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: 084335/166
;  CURRENT APPLICATION NUMBER: US/11/214,063A
;  CURRENT FILING DATE:  2005-08-30
;  PRIOR APPLICATION NUMBER: US/10/292,798
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: 10/017,161
;  PRIOR FILING DATE: 2001-12-18
;  PRIOR APPLICATION NUMBER: JP 2001-246789
;  PRIOR FILING DATE: 2001-06-18
;  NUMBER OF SEQ ID NOS: 2070
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1715
;   LENGTH: 10948
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   LOCATION: source
;   FEATURE:
;   LOCATION: (1)..(10948)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (201)..(572)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1011)..(1148)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1986)..(2325)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2353)..(2484)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2638)..(2820)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3675)..(3857)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4320)..(4429)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4632)..(4697)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4867)..(4992)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (5152)..(5228)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (5316)..(5379)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (5492)..(5577)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (5753)..(5810)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (6327)..(6431)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7312)..(7406)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7489)..(7557)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7741)..(7845)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9174)..(9447)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10656)..(10748)
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (6983)..(7082)
;   OTHER INFORMATION: a, t, c, g, unknown or other
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (9991)..(9991)
;   OTHER INFORMATION: a, t, c, g, unknown or other
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (10873)..(10873)
;   OTHER INFORMATION: a, t, c, g, unknown or other
US-11-214-063A-1715

  Query Match             3.4%;  Score 179.4;  DB 11;  Length 10948;
  Best Local Similarity   78.0%;  Pred. No. 3.1e-34;
  Matches  216;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy       1288 GGTCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTC 1347
              | || ||  |  |  |     ||||    |   | || ||||||||||| ||||||||||
```

```
Db       1481 GCTCCGTCACCCAGGCTGGAGTGTAGTGGCGCGATCTCAGCTCACTGCACCCTCTGCCTC 1540

Qy       1348 CCAGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCGCACGC 1407

Db       1541 CTGGGTTCAAACAATTCTCGTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGTGTGTAC 1600

Qy       1408 CCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGCTGGTCT 1467

Db       1601 CCGGCTAATTTTTGTATTTTAGTGGAGATGGGGTTTCACCATGTTGGCCAGGCTAGTCT 1660

Qy       1468 TGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGATTACAGG 1527

Db       1661 TGAACTCCTGACCTCAGGTGACCCACCTGCCTCGGACTCCCAAAGTGCTGGGATTACAGG 1720

Qy       1528 CATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAA 1564

Db       1721 CATGAGCCACTGCACCAGACCCCACCTCAGTTTCTGA 1757
```

RESULT 12
US-10-868-184C-6360/c
; Sequence 6360, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6360
; LENGTH: 6708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-184C-6360

Query Match 3.4%; Score 179.2; DB 6; Length 6708;
Best Local Similarity 77.9%; Pred. No. 2.9e-34;
Matches 232; Conservative 0; Mismatches 58; Indels 8; Gaps 1;

```
Qy       1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349

Db       3909 TCTGTCTCTCAGGCTGGAGTACAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC 3850

Qy       1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG------- 1402

Db       3849 AGGTTCAAGTAATTCTCCTGCCTCAGCCTCCCGAGTAGCGGGGATTACAGGTGCCCAACA 3790

Qy       1403 -CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461

Db       3789 CCACACATGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGTTAGCCAGGC 3730

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521

Db       3729 TGGTCTTGAACTCCTGACCTCAGATGATCCGCCTGCCTCGGCCTCTCAAAGTGCTGGGAT 3670

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579

Db       3669 TACAGGCATGAGCCATCGCACCCAGCCTATGGTACACCTTTACTGAGGAAACAATTCA 3612
```

RESULT 13
US-10-868-184C-11267/c
; Sequence 11267, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06012
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06058
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06044
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11267
; LENGTH: 6708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-184C-11267

Query Match 3.4%; Score 179.2; DB 6; Length 6708;
Best Local Similarity 77.9%; Pred. No. 2.9e-34;
Matches 232; Conservative 0; Mismatches 58; Indels 8; Gaps 1;

```
Qy       1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349

Db       3909 TCTGTCTCTCAGGCTGGAGTACAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC 3850

Qy       1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG------- 1402

Db       3849 AGGTTCAAGTAATTCTCCTGCCTCAGCCTCCCGAGTAGCGGGGATTACAGGTGCCCAACA 3790

Qy       1403 -CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461

Db       3789 CCACACATGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGTTAGCCAGGC 3730

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521

Db       3729 TGGTCTTGAACTCCTGACCTCAGATGATCCGCCTGCCTCGGCCTCTCAAAGTGCTGGGAT 3670

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579

Db       3669 TACAGGCATGAGCCATCGCACCCAGCCTATGGTACACCTTTACTGAGGAAACAATTCA 3612
```

RESULT 14

```
US-10-868-184C-6360/c
; Sequence 6360, Application US/10868184C
; GENERAL INFORMATION:
;  APPLICANT: Rosen, et. al
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS805
;  CURRENT APPLICATION NUMBER: US/10/868,184C
;  CURRENT FILING DATE:  2004-06-16
;  PRIOR APPLICATION NUMBER: 60/278,650
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/833,245
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US01/11988
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US00/06043
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06012
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06058
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06044
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06059
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06042
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06014
;  PRIOR FILING DATE: 2000-03-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13046
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6360
;    LENGTH: 6708
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-868-184C-6360

  Query Match             3.4%;  Score 179.2;  DB 7;  Length 6708;
  Best Local Similarity   77.9%;  Pred. No. 2.9e-34;
  Matches  232;  Conservative    0;  Mismatches   58;  Indels    8;  Gaps    1;

Qy       1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349
             ||||| ||| |  |     |  |    | || ||||||||||||||||||||||||||||
Db       3909 TCTGTCTCTCAGGCTGGAGTACAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC 3850

Qy       1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG------- 1402
             |||||||||| |||||||||| |||||||||||| ||||| |||| ||||||  |
Db       3849 AGGTTCAAGTAATTCTCCTGCCTCAGCCTCCCGAGTAGCGGGGATTACAGGTGCCCAACA 3790

Qy       1403 -CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461
              ||| |  ||||||||||||||||| ||||||||||||||||||  |||| ||||||  |||
Db       3789 CCACACATGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGTTAGCCAGGC 3730

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
             |||||||||||||||||||||| ||||||  ||  |||| |||||  ||||||||||||
Db       3729 TGGTCTTGAACTCCTGACCTCAGATGATCCGCCTGCCTCGGCCTCTCAAAGTGCTGGGAT 3670

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
             |||||||||||| || ||| ||| ||| | |||     |||| | |||||  | || |
Db       3669 TACAGGCATGAGCCATCGCACCCAGCCTATGGTACACCTTTACTGAGGAAACAATTCA 3612


RESULT 15
US-10-868-184C-11267/c
; Sequence 11267, Application US/10868184C
; GENERAL INFORMATION:
;  APPLICANT: Rosen, et. al
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS805
;  CURRENT APPLICATION NUMBER: US/10/868,184C
;  CURRENT FILING DATE:  2004-06-16
;  PRIOR APPLICATION NUMBER: 60/278,650
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: 09/833,245
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US01/11988
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: PCT/US00/06043
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06012
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06058
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06044
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06059
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06042
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: PCT/US00/06014
;  PRIOR FILING DATE: 2000-03-09
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13046
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11267
;    LENGTH: 6708
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-868-184C-11267

  Query Match             3.4%;  Score 179.2;  DB 7;  Length 6708;
  Best Local Similarity   77.9%;  Pred. No. 2.9e-34;
  Matches  232;  Conservative    0;  Mismatches   58;  Indels    8;  Gaps    1;

Qy       1290 TCTGTGTCTTACACCTACCTGTATGCTCTACACCTGAGCTCACTGCAACCTCTGCCTCCC 1349
             ||||| ||| |  |     |  |    | || ||||||||||||||||||||||||||||
Db       3909 TCTGTCTCTCAGGCTGGAGTACAGTGGCACAATCTCAGCTCACTGCAACCTCTGCCTCCC 3850

Qy       1350 AGGTTCAAGCAATTCTCCTGTCTCAGCCTCCCGCGTAGCTGGGACTACAGGCG------- 1402
             |||||||||| |||||||||| |||||||||||| ||||| |||| ||||||  |
Db       3849 AGGTTCAAGTAATTCTCCTGCCTCAGCCTCCCGAGTAGCGGGGATTACAGGTGCCCAACA 3790

Qy       1403 -CACGCCCGGCTAATTTTTGTATTGTTAGTAGAGATGGGGTTTCACCATATTAGCCCGGC 1461
              ||| |  ||||||||||||||||| ||||||||||||||||||  |||| ||||||  |||
Db       3789 CCACACATGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGTTAGCCAGGC 3730

Qy       1462 TGGTCTTGAACTCCTGACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGAT 1521
             |||||||||||||||||||||| ||||||  ||  |||| |||||  ||||||||||||
Db       3729 TGGTCTTGAACTCCTGACCTCAGATGATCCGCCTGCCTCGGCCTCTCAAAGTGCTGGGAT 3670

Qy       1522 TACAGGCATGAGTCACCGCGCCCGGCCAAGGGTCAGTGTTTAATAAGGAATAACTTGA 1579
             |||||||||||| || ||| ||| ||| | |||     |||| | |||||  | || |
Db       3669 TACAGGCATGAGCCATCGCACCCAGCCTATGGTACACCTTTACTGAGGAAACAATTCA 3612


Search completed: January 26, 2006, 09:25:03
Job time : 762 secs
```